



1998

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QY 3901 ACGATGACTCGCGCTTCGGCAAGGATGGGCAATTTACGACTGAAAACCTTTTCAATTA 3960  
Db 3961 ttgaaaaataaatttttgaacacgctgttatcactatgatttttaagtagtgcttagctt 4020  
QY 3961 TTGAAAAATAATATTTTGAACACGCTGTATACATATGATTTTAAATGAGTAGCTTAGCTT 4020  
Db 4021 tggcattagaagatgtacatctgcccacaaagaccatactcagagatatatttatactata 4080  
QY 4021 TGGCAATTAGAAGATGTACATCTGCCACAAAGACCCTACTCGAGGATATTTTATACTATA 4080  
Db 4081 tggacagaatatttacggttatattcttcttggaatgttaatacaagtgggtgcgctcg 4140  
QY 4081 TGGACAGAATATTTACGGTTATATCTCTTGGAAATGTTTAAATCAAGTGGTGGCGCTCG 4140  
Db 4141 gcttcaaaagtgtacttaccacacgctggtgtgttgctcgatttctgattgctatggtat 4200  
QY 4141 GCTTCAAAAGTGTACTTCAACACGCTGCTGTGGCTCGATTTTCTGATGTCATGCTAT 4200  
Db 4201 cgttatcaaatcgttcttcaacttcttcaacttcttgagctggttggttatccaagccttcaagacta 4260  
QY 4201 CGCTTATCAAGCTCGTTCCTTCACTTGTGTGAGCTGTGTGTATTCAGGCTTCAAGACTA 4260  
Db 4261 tgcgaacgttaagacactagacacactacgtgcacgtcccgatcccgatcagggcagtgaagg 4320  
QY 4261 TCGAACGTTAAGAGCATGAGACCATGACCTACCTGCGCATGTCCGCTATGACGGGCTAGAGG 4320  
Db 4321 tctgttctaagctgctggttaacaaagctaaccgttccatcttcaatgtgctattggtgtgc 4380  
QY 4321 TCGTGTAAATGCGCTGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTTGCTGTGTC 4380  
Db 4381 taatttttgctaaatttttgccataatggtgtgtacagcttttttgcggaaaaattttta 4440  
QY 4381 TAATATTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTGTGTGAAAAATATTTTA 4440  
Db 4441 agtcgaggacatgaatggcagcagctcagccagagatcataccaaatcgcaatccct 4500  
QY 4441 AGTCGAGGACATGAATGGCAGAGCTACGCCAGAGATCATACCAATGCCAATGCCCT 4500  
Db 4501 gcgagagcagaactacacgtgggtggaattcagcaatgaatttcgatactatgagtaacg 4560  
QY 4501 GCGAGAGCGAGAACTACACGCTGGTGAATTCAGCAATGAATTTTCGATCATGTAGTAAAG 4560  
Db 4561 cgtatctgctcttccaaagtggccaccttcaaggctggtgatacaaatcaatgaacgatg 4620  
QY 4561 CGTATCTGTGCTTTTCCAAAGTGCCACCTTCAAAAGGCTGGATACAAATCATGAACGATG 4620  
Db 4621 ctatcgattccagaggttgacaagaacaacaaatctgtgaacgaacatctacatgtatt 4680  
QY 4621 CTATCGATTACAGAGGTGACAGCAACCAATTCGTGTGAACCAACATCTACATGTATT 4680  
Db 4681 tatatttgattcttcatcatatttgatcttttccactcaactcaactgttcttattggtg 4740  
QY 4681 TATATTTCGTATTCTTCATCATATTTTGGATCTTTTTCACACTCAATCTGTTCAATTGGTG 4740  
Db 4741 ttatcattgataatttttaagtacaaagaaaaagcaggtgggtgattcattagaaattgttca 4800  
QY 4741 TTATCATTGATAATTTTAAATGAGCAAAAGAAAAAGCAGGCTGGATCATTAGAAATGTTCA 4800  
Db 4801 tgacagaagatcagaaaagtactataatgctatgaaaaagatgggtctctaaaaaacat 4860  
QY 4801 TGACAGAGATTCAGAAAAGTACTATATGTCTATGAAAAGATGGGCTCTAAAAAAGCAT 4860  
Db 4861 taaagccattccaagccaaggtggcgaccacacaagcaatagttctttgaaatagtaacgg 4920  
QY 4861 TAAAGGCCATTTCCAAAGACCAAGGTGGCGACCAACCAAGCAATAGTCTTTGAAATAGTAACCG 4920

Db 4921 ataagaattcgcataataatcattatgtatttattcattggtctgaacatgttccaccatgaccc 4980  
QY 4921 ATAAGAAATCGATATAATCATATTATGTTATTATTCATTGCTGTAACATGTTCCACATGACCC 4980  
Db 4981 tccatcgttacgactgcctcgacacgcatgaacgctgcttagactacttcaatgcgatat 5040  
QY 4981 TCGATCCTTACGATGCTCGGACACGCTATACGCGGTCTTAGACTATCTCAATGCGGATAT 5040  
Db 5041 tctgagtattttccagttccgaaatgtctattaaaaaaatttcgcgttttacgataatacactt 5100  
QY 5041 TCGTAGTATTTTTCAGTTCCGAATGCTATATAAAATATTCGCTTTCAGGATATCACTATT 5100  
Db 5101 ttattgaccattggaatttattttagtagtagttagtgcatttttatccattttaggttctg 5160  
QY 5101 TTATTGAGCCATGGAATTTATTGATGTAGTAGTGTGTCATTTTATCCATTAGTCTTGGTCTTG 5160  
Db 5161 tacttagcgatatattcagaaagtacttgcgtcgacgacctcctcgagtaggtgcgtg 5220  
QY 5161 TACTTAGCGATATTTATCGAAGTACTTCTGTGCGCGACCCCTGCTCCGAGTGGTGGTG 5220  
Db 5221 tggcgaaagtgggcccgtgtccttcgactggtgaaggagcgaaggcgcatcggacactgc 5280  
QY 5221 TGGCGAAGTGGGCCGTGCTCTTCGACTGCTGAAGGAGGCAAGGGCATTCGGACACTGC 5280  
Db 5281 tcttcgcttggccatgtcgtcgtccgcccctgttccaacatctgcctgctgctgttctctgg 5340  
QY 5281 TCTTCGCGTTGGCCATGCTGCTCGCGCCCTGTTCACATCTGCCTGCTGCTGTTCCTCG 5340  
Db 5341 tcatgttcatctttgccattttggcgatgctgttccatgcacgtaaggaagaagagcg 5400  
QY 5341 TCATGTTCACTTTGGCAATTTTCGGCATGCTGCTTTCATGSCACGTGAAGGAGAAGCG 5400  
Db 5401 gcaataacgacgctctacaacttcaagacctttggccagagcatgactcctctttcaga 5460  
QY 5401 GCATTAACGAGCTCTACAACCTTCAAGACCTTTGGCCAGAGCATGATCTCTCTTCAGA 5460  
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QY 5461 TGTCGAGCTCAGCGGTTGGGATGGTGTACTGGACGCGCATATCAATGAGGAAGCATGCG 5520  
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QY 5521 ATCCACCCGACAGCGACAAAGGCTATCCGGGCAATTTGTGTTTTCAGCGACCGTTGGAAATA 5580  
Db 5581 cgttctcctctcatacctagttataagctttttagtagttataatgatacatgctg 5640  
QY 5581 CGTTTCTCTCTCATACCTAGTTTAAAGCTTTTGTATGTTTAAATATATGATGCTGCTG 5640  
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QY 5641 TCATTTCTCGAAGAACTATAGTCAGGCCACCCAGGACGCTGCAAGAGGGTCTTAACCGACGACG 5700  
Db 5701 actacgacatgactatgagatctggcagcaattcgatcccgaggggcccaccagtagtaac 5760  
QY 5701 ACTACGACATGTACTATGAGATCTGCGAGCAATTCGATCCGAGGGCACCCAGTACATAC 5760  
Db 5761 gctatgacagctgctcgaattcttgacgtactgagcccccgctgacagatccacaac 5820  
QY 5761 GCTATGATCAGCTGTCCGAATTTCTGGACGTACTGAGCCCCCGCTGCGATCCACAAAC 5820  
Db 5821 cgaaagtaacaaagatcatatcgatggacatacccatctgtcgtcgttgacctcatgtact 5880  
QY 5821 CGAAACAAGTACAAGATCATATCGATGACATACCCATCTCTCGCGGTGACCTCATGTACT 5880  
Db 5881 gctcgacatcctcgcagcccttacaaagactcttcttgcggaaaggggcaatcccgatag 5940  
QY 5881 GCCTCGACATCTTCGACGCCCTTACGAAAGACTTCTTTGCGGGAAGGGCAATCCGATAG 5940  
Db 5941 aggagcgggtgagattggtgagatagcgcccgccgacatagagggctacgaccccg 6000  
QY 5941 AGGAGACGGGTGAGATTGGTGAGATAGCGGCCCGCCGGATACGGAGGGCTACGAGCCCG 6000



Db 5004 ctcaattgttggaactgtctctccgacatcatcacaagaagtacttcttctccccgacact 5063  
QY 5144 ATCCATCTTAGGTTGTGTTACTTAGCATATATCGAGAAGTACTTCGTGTCGCCGACCTT 5203  
Db 5064 ctcccggtgtaactcgtctgcccagagatcgccgcatctcagctgatacggagccaa 5123  
QY 5204 GCTCCGAGTGGTGGTGGGAAAGTGGGCGGTGCTTCGACTGGTGAAGGGAGCCAA 5263  
Db 5124 gggattcgcacgtgtctctccctcatgatgtccctgctccgcccgcctctcaacatcg 5183  
QY 5264 GGGATTCGGACATGCTCTCTCGGTGGCCATGTCGTCGCGGCCCTGTTCAACATCTG 5323  
Db 5184 cctcctctctctcgtctgtaactctactctactctctctctctctctctctctctct 5243  
QY 5324 CTTGCTCTCTCTCTGCTGTAATCTCTTGGCAATTTTCGGCATGCTCTTCTTCTTCA 5383  
Db 5344 cgtcaagtggagggcggcgtatgacatgttcaacttccagactcgcgcaacagat 5303  
QY 5384 CGTGAAGGAGAGAGCGCATTAACGACGCTACACATCTCAAGACCTTTGGCCAGAGCAT 5443  
Db 5304 gctgtgctgttccagatacacacatcagcggcgtgggacgctcctcctcagcccatcct 5363  
QY 5444 GATCTGCTCTCTTCAGATTCGACGCTCAGCGGTTGGGATGCTGACGAGCGCATTTAT 5503  
Db 5364 caacacggggcctccctactcgcaccccaacactgcccaacagcaacggtcctccggggaa 5423  
QY 5504 CAAT--GAGGAAGC--A-TGGATGCC--ACCCGAC-AGCGACAAGGCTATCCGGGCAA 5554  
Db 5424 ctgtggagcccggtgggtggatcctctcttccaccacccatcacatctctctctct 5483  
QY 5555 TTGTGGTTCAGGCGACGCTTGGAAATACGTTCTCTCTCATACCTAGTTATAAGCTTTT 5614  
Db 5484 catcgtgttcaacatgtacatcgcacatcctcctcagaaactcagcgtggtccacagga 5543  
QY 5615 GATAGTTATTATATGTACATTCCTGTCATTCGAGAACTATATGTCAGGCGCACCGAGA 5674  
Db 5544 gacacagagccctgagcggagcactctcagatgtctctatgatctctgagagaagt 5603  
QY 5675 CGTGAAGAGGCTCTAACCGAGCAGCTACGACATGCTACTATGAGATCTTGGCAGCAAT 5734  
Db 5604 cgaaccgagggcaccacagttcattgagatctggtccctctcagacttgcagatgctt 5663  
QY 5735 CGATCCGAGGCGACCCAGTACATACGCTATGATGATGCTGCTGCCAATCTCGGAGTACT 5794  
Db 5664 gtctgagcgtctccgcatcgcaccccaacacacagataagcctcacaatgatctgct 5723  
QY 5795 GGAGCCCGCTGCAGATCCACAAACCGACAGTACAGATCATATCGATGGACATACC 5854  
Db 5724 catggtgagcggagacogtaccactgtatggacatactgttgcgttccacca 5777  
QY 5855 CATCTGTCGGGTGACCTCATGTACTGCTGACATCCTCGAGCGCCTTACGAA 5908

RESULT 4  
ID Q05831 standard; cDNA; 7555 BP.  
AC Q05831;  
DT 10-JAN-1991 (first entry)  
DE Cardiac sodium channel gene.  
KW Rat; arrhythmia; ss.  
OS Rattus rattus.  
PN W09009391-A.  
PD 23-AUG-1990.  
PF 09-FEB-1990; U00768.  
PR 13-FEB-1989; US-310330.  
PA (ARCH-) ARCH DEV CORP.  
PI Rogart RB;  
DR WPI; 90-275095/36.  
DR P-PSDB; R06584.  
New rat cardiac sodium channel proteins - and associated DNA sequences, polypeptides and peptides associated with arrhythmias, useful as antiarrhythmic and cardiotoxic drugs. 1; 65pp; English.

CC The sequence is derived from 3 overlapping clones, PRH3-1, PRH4-23, and PRH14-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)  
CC The clones were isolated from a cDNA library in the lambda zap vector prep. from mRNA obtd. from newborn rat hearts using rat brain II cDNA probe. The isolated DNA can be used to screen a similar human derived cardiac cDNA library for the corresponding human gene. Proteins produced by expression of the DNA have diagnostic therapeutic, and prognostic applications.  
SQ Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;  
Query Match 5.3%; Score 344; DB 1; Length 7555;  
Best Local Similarity 63.3%; Pred. No. 1.63e-215;  
Matches 1174; Conservative 0; Mismatches 650; Indels 30; Gaps 19;  
Db 3927 ggaacaagtgttccactcagctcttgttggagatgctgctcaagtgggtggctacgg 3986  
QY 4082 GCACAGAAATATTACGGTTATATCTTCTTGGAAATGTTAATCAAGTGGTGGCGCTCG 4141  
Db 3987 ctccaagaagtacttccacaacgctggtgctgctggacttctctgattgtgagctctc 4046  
QY 4142 CTTCAAGTGTACTTCCCAACGCGTGGTGGTGGCTCGATTTCGTGATGTGTCATGTC 4201  
Db 4047 gctggttcagcctctggtgcaaacacaccttagcttccgcaaatgggtcccatcaagt 4106  
QY 4202 GCTTATCAACTTCGTTGCTTCACTTGTGGAGCTGGTGTTCAGCCCTTCAAGACTAT 4261  
Db 4107 gaggacactgctgcaacttcgacctgagggccttctgctgagatttgaggcctcggt 4166  
QY 4262 GCAGCGTTAAGAGCACTGAGACCACTAGTCCCATGTCCTGATGTCAGGCACTGAGGGT 4321  
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QY 4322 CGTCTTAATGCGTGGTACAAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGCT 4381  
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QY 4382 AATATTTTGGCTAAATTTTGGCATAAATGGGTGTACAGCTTTTTCGGAATAATTATA 4441  
Db 4287 gtgcacacacagacagaggggacctgctctgaactacacacctctgtaacaacaagag 4346  
QY 4442 GTGCCAGGAC--AT-GAATGGCAGGAAGCTCAGC-C-ACGAGATCATACCAATCGCAA 4495  
Db 4347 tgaatgagtccttcaacgtgacggagaggtgtgacttgacggcagcagcagtggaagc 4406  
QY 4496 TGCTTGCAGAGCGAGAAC-T-ACAGCTGGGT-CAATTC-AGCAA--TGAATTCGA--- 4546  
Db 4407 tgaacaactggagccgggtacctgcccctcctgagctgagctgacatttaaaagctgag 4466  
QY 4547 T--CAT-GTAGGTAAACGCTATCTGTCCTTTTCCAAAGTGGCCACCTTCAAGGCTGGAT 4603  
Db 4467 ggaacatgctgctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 4526  
QY 4604 ACAATCATGAACGATGCTATCGATTCCAGAGGTTGGCAACCAACCAATTCGTGAAC 4663  
Db 4527 caacctacatgtacatctacttctgcttcttcttcttcttcttcttcttcttcttctt 4586  
QY 4664 GAACATCTACATGATTATATTCTGTTATTTCTTCATCATATTTGGATCTCTTTTACACT 4723  
Db 4587 caaccttctcagctggtgctcattgtcgtcttcaaccagcagaagaagaagtaggggg 4646  
QY 4724 CAATCTGTTCAATGGTGTATCATTAATTTAATGAGCAAAAGAAAAGAGAGAGTGG 4783  
Db 4647 c-cag--gatatcttcagcggagagcagaagaagtactcaatgacctgaagaagct 4703  
QY 4784 ATCATTAGAAATGTTTCAGACAGAGTACAGAAAAGTACTATATGCTATGAAAAGAT 4843  
Db 4704 gggctcaagaaccccaagcccatccacggccttgaacagtagtaccaggggtttcat 4763  
QY 4844 GGGCTTAATAAACCATTAAAGCCATTCCAGACCAAGGTGGCGACCAACAGCAATAGT 4903  
Db 4764 attcgacattgtgacaacagcagccttcctgctgacacatcatgttccctcctgtttgaa 4823  
QY 4904 CTTTGAATAGTAACCGATAAGAAATTCGATATATCATTAATGTTATTATGTTGCTGAA 4963

hypotensive; antiinflammatory; trauma; pain; neurological disorder;  
antisense; gene therapy; ss.

Key Conflict Location/Qualifiers

FT conflict 1

FT /tag= a

FT /note= "T30193 contains G at this position"

FT 697..1665

FT /tag= b

FT /note= "Probe used in differential tissue

FT expression studies"

FT complement (1132..1151)

FT /tag= c

FT /note= "Binds primer T30196"

FT 1495..1518

FT /tag= d

FT /note= "Binds primer T30197"

PN WO9614077-A1.

PD 17-MAY-1996.

PF 02-NOV-1995; U14251.

PR 07-NOV-1994; US-334029.

PR 07-JUN-1995; US-482401.

PA (TROP-) TROPHIX PHARM INC.

PA (UNY ) UNIV NEW YORK STATE RES FOUND.

PI Borden LA, Halesgoua S, Mandel G;

DR WPI; 96-251547/25.

DR P-PSDB; R99638.

PT Nucleic acid encoding peripheral nervous system specific sodium

PT channel peptide - useful for sodium channel-associated disease or

PT trauma.

PS Claim 2; Fig 7; 80pp; English.

CC The sequence encodes repeat domain-II of a rat peripheral nervous

CC system sodium channel peptide-1 alpha-subunit (PN1), with sodium

CC channel activity, and has been isolated from a rat PC12 subclone

CC PKI-4 cell culture, expressing high levels of cAMP-dependent

CC protein-kinase-inhibitor. A cDNA library has been screened with

CC primers T30196-97, and the product has been used as a probe to

CC re-screen the library to isolate this sequence. The full-length

CC gene is given in T30193. A probe derived from the sequence may be

CC used in differential tissue expression studies. The peptide may be

CC used to isolate sodium-agonists and sodium-antagonists for use as

CC analgesics, hypotensives, antiinflammatories, and in therapy of

CC sodium channel-associated pathology or trauma, e.g. neurological

CC disorders. The DNA (in sense or antisense orientation) may be used

CC in gene therapy.

CC Sequence 3033 BP; 860 A; 689 C; 687 G; 797 T;

Db 4824 catgtgaccatgatgttgagacagatgacacagccctgagaaggtcaacatcttggc 4883

Qy 4964 CATGTCACCATGACCCCTCGATGTTACGATGCTGGGACACGTATAACGCGGTCTAGA 5023

Db 4884 caagatacaactctctcttgccatctcttcacagcgagtgattgtcaagatggctgc 4943

Qy 5024 CTATCTCAATGCGATATCTAGTATTTTCAGTTCCGATGCTCTATTAATAATATTCG 5083

Db 4944 cctgcgcactattacttcacacagctggaacatctctgaactttgtgtgtgctatcct 5003

Qy 5084 TTTACGATATCACTATTTATTGAGCCATGGAATTTATTGATGATAGTAGTTGTCATTTT 5143

Db 5004 ctccattgttggcactctctctccgcacatcaccagaagtaactctctcccccacat 5063

Qy 5144 ATCCATCTTAGTCTTACTTAGCATATATATGAGAACTACTCGTTCGCGGACCTT 5203

Db 5064 ctccgggttcactctgctgcagagatcgccgcactctcaggctgatccgcggagccaa 5123

Qy 5204 GCTCGAGTGTGGTGTGGCGAAGTGGCGCGTGTCTTCGACTGGTGAAGGAGGCCAA 5263

Db 5124 ggggattcgacgctgtcttccctccatgatgtccctgcgcgcctcttcaacatcgg 5183

Qy 5264 CGGCATTGCGACACTGCTCTTCGGTGTGGCCATGCTGCGCGCCCTGTTCACATCTG 5323

Db 5184 cct 5243

Qy 5324 CTTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5383

Db 5244 cgtcaagtggagcggcgatgatgatgatgatgatgatgatgatgatgatgatgatgat 5303

Qy 5384 CTTGAGGAG 5443

Db 5304 gctgtgtctgttccagatcaccacacagcggctgagcggctcctccagcccatcct 5363

Qy 5444 GATCTGCTCTTTTCAGATCTGACGCTGACGCGGTGGGATGCTGCTGCTGCTGCTGCT 5503

Db 5364 caacacgggctcctctctctcgcacccacacacacacacacacacacacacacacac 5423

Qy 5504 CAAT--GAGGAGC--A-TGGGATCC--ACCGAC-AGCGACAAAGGCTATCCGGGCAA 5554

Db 5424 ctgtggagcggcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 5483

Qy 5554 TTGTTGTTACGACGACGCTTGGGATACGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5614

Db 5484 catcgtgttcaacatgatctacacacacacacacacacacacacacacacacacacac 5543

Qy 5615 GATAGTTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5674

Db 5544 gagcacagagcctctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 5603

Qy 5675 CGTCAAGAGGGTCTAACCGACGACGACGACGACGACGACGACGACGACGACGACGACG 5734

Db 5604 cgacccggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5663

Qy 5735 CGATCGGAGGGCACCAGTACATACGCTATGATGATGATGATGATGATGATGATGATGAT 5794

Db 5664 gtcgagcgtctcgcacgcacacacacacacacacacacacacacacacacacacac 5723

Qy 5795 GGAGCCCGCTGAGATCCCAACACCGAAGTACAGATCATATCATGATGACATAC 5854

Db 5724 catggtgagcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5777

Qy 5855 CATCTGCGCGGTGACCTCATGTACTGCTGCGATCTCTGCGACGCGCTTACGAA 5908

RESULT 5

ID T30192 standard; cDNA; 3033 BP.

AC T30192;

DT 25-OCT-1996 (first entry)

DE Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.

KW Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;

sodium-agonist; sodium-antagonist; drug screening; analgesic;



[illegible]

Db	2173	aaatttgagacttttggcaacagcatgatctgttggttccaaataccaccctctgcggc	2233
Qy	5418	AACTTCAAGACCTTTGGCCAGGACATGATCTGTCTTTTCAGATGTGAGGTGAGCGGT	5477
Db	2233	tgggacgggactgctggcccccatcctcaacagcgcacctccgactgtgacctaataaaa	2292
Qy	5478	TGGATGGTGTACTGGACGCCATTAATCAATGAGGAACATGCGA-TCC-ACCCGACGC-	5534
Db	2293	gttcaccacggaagtctcagtgaagggactgtgggaaccacatccgtggggatttttac	2352
Qy	5535	GA-CAA--AGGCTATCCGG-GCAATG--TG-GTTCAGCGA-CCGTTGGAATAACGTTT	5585
Db	2353	ttttcgagctacatcatcatctctctctgtgtgtgtgtgaaatcatcatcgctgtcatc	2412
Qy	5586	CTCCTCTCATACCTAGTATTAAAGCTTTTGTAGTAGTTAATAATGTACATGTGCTCAT	5645
Db	2413	ctggagaacttcaggtcgccaccgaagagacactgagctctgagtggagcagcttt	2472
Qy	5646	CTCAGAGAACTATAGTCAGGCGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGAGCTAC	5705
Db	2473	gagatgtctacagaggtctctgggagaagttcgaccctgacgcacactcagtttoatagttc	2532
Qy	5706	GACATGTACTATGAGTCTGGCAGCAATTCGATCGGAGGGCCACCGATACATACGCTAT	5765
Db	2533	tgcaagctctctgactttgcagctgccccggatctccctccctcatcgcgaacccaaac	2592
Qy	5766	GATCAGCTGTCCGAATTCCTGGGACGTACTGGAGCCCCCGCTGCAGATCCACAAACCGAAC	5825
Db	2593	aaagtcagctcattgcatcggaccctgcccattggtagtggagacgcgcacactgctgtg	2652
Qy	5826	AAAGTACAAGATCATATCGATGGACATACCCATCTGTGCGGGTGACCTCATGTACTGCTC	5885
Db	2653	gacatctgtttgtctttacaaa	2675
Qy	5886	GACATCCTCGAGCGCCTTACGAA	5908
RESULT	6		
ID	T30193	standard; DNA; 6452 BP.	
AC	T30193;		
DC	25-OCT-1996 (first entry)		
DE	Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.		
KE	Rat; peripheral nervous system; sodium channel; PN1; PC12; PK1-4;		
KW	sodium-agonist; sodium-antagonist; drug screening; analgesic;		
KW	hypotensive; antinflammatory; trauma; pain; neurological disorder;		
KW	antisense; gene therapy; ss.		
OS	Rattus rattus.		
PH	Key	Location/Qualifiers	
FT	cds	326..6280	
FT		/*tag= a	
FT		/product= Full-length PN1 protein	
FT	conflict	3185	
FT		/*tag= b	
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FT	misc_feature	3185..6217	
FT		/*tag= c	
FT		/note= "Fragment T30192 (claim 2)"	
FT	misc_feature	3881..4847	
FT		/*tag= d	
FT		/note= "Probe used in differential tissue expression studies"	
FT	primer_bind	complement (4316..4335)	
FT		/*tag= e	
FT		/note= "Binds primer T30196"	
FT	primer_bind	4679..4702	
FT		/*tag= f	
FT		/note= "Binds primer T30197"	
PN	W09614077-A1.		
PD	17-MAY-1996.		
PF	02-NOV-1995; U14251.		
PR	02-NOV-1994; US-334029.		
PR	07-JUN-1995; US-482401.		

PA	(TROP-) TROPHIX PHARM INC.	
PI	(UINY ) UNIV NEW YORK STATE RES FOUND.	
PI	Borden LA, Halegoua S, Mandel G;	
WPI	96-251547/25.	
DR	P-PSDB: R99639.	
PT	Nucleic acid encoding peripheral nervous system specific sodium	
PT	channel peptide - useful for sodium channel-associated disease or	
PT	trauma.	
PS	Example 1; Fig 9; 80pp; English.	
CC	The sequence encodes a rat peripheral nervous system sodium channel	
CC	peptide-1 alpha-subunit (PNI), with sodium channel activity, and	
CC	has been isolated from a rat PC12 subclone PKI-4 cell culture,	
CC	expressing high levels of cAMP-dependent protein-kinase-inhibitor.	
CC	A cDNA library has been screened with primers T30196-97, and the	
CC	product has been used as a probe to re-screen the library to	
CC	isolate the fragment given in T30192. This has been used to isolate	
CC	the full-length gene. A probe derived from the sequence may be	
CC	used in differential tissue expression studies. The peptide may be	
CC	used to isolate sodium-agonists and sodium-antagonists for use as	
CC	analgesics, hypotensives, antiinflammatories, and in therapy of	
CC	sodium channel-associated pathology or trauma, e.g. neurological	
CC	disorders. The DNA (in sense or antisense orientation) may be used	
CC	in gene therapy.	
SO	Sequence 6452 BP; 1816 A; 1454 C; 1550 G; 1632 T;	

Query Match	4.8%	Score 312;	DB 21;	Length 6452;
Best Local Similarity	62.3%	Pred. No. 1.01e-192;		
Matches 1210;	Conservative	0;	Mismatches 700;	Indels 33;
Gaps 21;				
Db	3920	atgctctcgcacgacgagggagctcgtgctgttgaagatcatctatattgaagaagaaaag	3979	
Qy	3996	ATGATTTTAAGTAGTAGCTTAGCTTGGCATTAGAAGATGTACATCTGCCACAAGACCC	4055	
Db	3980	accattaagattactcggagatagtgcacaagattattcaccatacatcttactcttgaa	4039	
Qy	4056	ATATCGCAGGATATTTTACTATATGACACAGATATTTACGGTATATTCTTCTTGAA	4115	
Db	4040	atgctctcaaatgggtcgcatatgggtataaaacattttcacataatgcctggtgttg	4099	
Qy	4116	ATGTTTAAACAAGTGTGGCGCTCGGCTTCAAGTGTAATTCACCAACGGCTGCTGTGG	4175	
Db	4100	ctggactcttcaattgttgatgtgtctctagttactcttagtagcaacacactcttggctac	4159	
Qy	4176	CTCGATTTGCTGATTGTCTATGCTATCGGTTATCAACTTCGTGTGCTTCACTTGTGGAGCT	4235	
Db	4160	tcagaccttggcccatataaactctcagcacactgagggcctaaagacccttaagagcc	4219	
Qy	4236	GGTGTGTAATCAAGCCTTCAAGACTATGCGAAGCTTAAGAGCACTGAGACCCTACGTGCC	4295	
Db	4220	ttgtctagatttgaaggaatgaggttagtggccaacgactcactataggagcaatccctcc	4279	
Qy	4296	ATGTCCTCGTATCAGGGCATAGGGTCGTCGTTAATGCGCTGGTACAAGCTATACCGTCC	4355	
Db	4280	atcatgaacgtgtctctcgtgtgccttataattctggctaataatttagcatcatggagtc	4339	
Qy	4356	ATCTTCAATGTCTATPTGTGTGTCTAATATTTTGGCTAAATTTTGGCCATTAATGGGTGA	4415	
Db	4340	aactcttttctggcgaagttctcatgagtgtgcaacaccacgagtggtgcacgatttctc	4399	
Qy	4416	CAGCTTTTCTCGGAANAATATTTTAAGTCGGAGGACATGA---ATGG--CACGAAGCTCA	4470	
Db	4400	acatctcaagttgcaaacggtcttgagtgttttgcctgatgaacggttagtggaatgtg	4459	
Qy	4471	GC--CAGGAGATCATACCAAAATCGCAATGCCT-GC---GA-GAGCGAGAACT-ACACGTG	4522	
Db	4460	cgatgaaaaacctgaaagtaaaacttcgacaaacgttggcttgggttaacctgtcgtcgtt	4519	
Qy	4523	GG-TG---AATTACAGCAA-TGNAATTTTCGATCATGTAGGTAAACCGGTATCTGTGCCTTTTC	4577	
Db	4520	caagttgcacaattcaaggsgctggatggatattatgtatgcagcaggttgaactgtttaat	4579	
Qy	4579	CAATCTCCCAACCTTCACAGCTGGATCAAAATCATGAACGATGCTATCGATCACGAGAG	4637	

Db	4580	gtaaatgaacagcgcgaataacacacagtcctctacatgtacatcttactttcgtcatcttc	4639
Qy	4638	GTGACAAGCAACCAATTCGTGAAGCAACATCTACATGTATTATTTATTCGTATTCTTC	4697
Db	4640	atcatcttcggctcaattctcagttgaacctgttcattcgggtgcacatagataatttc	4699
Qy	4698	ATCATATTGGATCCCTTTTTCACACTCAATCTGTTCTATGGTGTTATCATTGATAATT	4757
Db	4700	aaccaacagaa-aaaaagcttggaggtca--agatatctttatgacagaagaacsgaag	4756
Qy	4758	AATGACAAAGAAAAAGCAGGTGGATCATTAGAAATGTTACGACGAAGATCAGAAA	4817
Db	4757	aaatactaatgcaatgaagaagctgggtccaaaaaacacacacacacacacacacg	4816
Qy	4818	AAGTACTATAATGTATGAAGAGATGGGTCTAANAACCATTAAGAAGCCATCCNAGA	4877
Db	4817	ccagggaacaattccaaaggatgatatattgacttagtcacaaaccaagcttttgatc	4876
Qy	4878	CCAAGTGGCAGCACAGCAATAGTCTTGAAATAGTAACCGATAAGAAATTCGATATA	4937
Db	4877	accatcaatggtttcttatatgctccaacatggtaaccatgatgtagaaaaaggggcaa	4936
Qy	4938	ATCATATTATGTATTTCATTTGGTCTGAACATGTTCCACATGACCCTCGATCGTTAGATCG	4997
Db	4937	actgagtcacatgattatggtttacactggatcaacatggtcttcattatctcttcaact	4996
Qy	4998	TCGGACACGATATAACCGCGTCTAGACTATCTCAATCGGATATTCGTAGTTATTTTCAGT	5057
Db	4997	ggggagtggtggaagtaactccctccacacataactactactcactcactggtggtgaac	5056
Qy	5058	TCCGAATGTCATTAAAAATATTCGTTTAGATATCACTATTTATTAGCCCATGGAAT	5117
Db	5057	atttggattttggtgtagtgcctccattgtaggaaatgttctcgtcgagatgata	5116
Qy	5118	TTATTGTAGTAGTAGTAGTGCATTTATCCATCTTAGTCTGTACTTAGCGATATATC	5177
Db	5117	gagaagatttcgtgccctaccctgttccagtcattcccgctggccaggatggaacga	5176
Qy	5178	GAGAAGTACTTCGTGTCGCCACCTGCTCCGAGTGGTGGCGTGTGGCGAAAGTGGCGCGT	5237
Db	5177	atctcagcctgatcaaaaggccgaaggatccgcactcgtctcttgcgttcttgcgtg	5236
Qy	5238	GTCCCTTCGACTGGTAGAGGGAGCCAAAGGCAATCCGACACTGCTCTTCTGGTCATGTTCA	5297
Db	5237	tccttcctcgcgtgtcaacatcgccctcgtcttctcgttggtcatgttcatctacgcc	5296
Qy	5298	TCGCTCGCGCCCTGTTCAACATCTGCCGTGCTGTTCTCTTCCAGATGTCGACGTCTAC	5357
Db	5297	atcttgggatgtccaaacttgcctacgttaaaaggagcgtggaattaatgacatgttc	5356
Qy	5358	ATTTTCCGGATGTCGTTCTTCATGACAGTGAAGGAGAGAGCGGCATTAACGACGTCTAC	5417
Db	5357	aacttggagactttggcaacagcatgctgctgttcccaatcaccaacctctccggc	5416
Qy	5418	AACTTCAAGACCTTTGGCCAGACATGATCCCTCTTTCAGATGTCGACGTGACGCCGT	5477
Db	5417	tgggacgagactgtggcccccatctccaacgcacctcccgactgtgacctaaaaaa	5476
Qy	5478	TGGGATGGTGTACTGGACGCCATTATCAATGAGGAGACATGCGA-TCC-ACCCGACAGC-	5534
Db	5477	gttcaacccagaagttcagtggaaggagactgtggaaacccatccgtgggattttttac	5536
Qy	5535	GA-CAA--AGGCTATCCGG-GCAATTG---TG-GTTCAGCGA-CCGTTGGAATAACGTTT	5585
Db	5537	tttgcagctacatcatatctctcgttgggtgggtgaacatgtacatcgctgctc	5596
Qy	5586	CTCCTCTCATACCTAGTTATAAGCTTTTTCATAGTTATTAATATGTACATTTGCTGTCATT	5645
Db	5597	ctggagaacttcagctctgcacccagaagacactgacctctgagttaggacgacttt	5656
Qy	5646	CTCAGAACTATATGTCAGGCCACCGAGGAGCTGCAAGAGGGGTCTAACCGACGACATC	5705
Db	5657	cagatgttctacagaggtctgggagaagtctgcacctgacgccactcagttcttagagttc	5716



Db	4837	ctgttccagatgccgtcttcgagatggccgaatcctacgtcttagtcaaaagagca	4896
Qy	5202	ctgcctccagatggctggtggcgaagtcggcgtgtcttcgactggtgaaggagcc	5261
Db	4897	aagggatccgcaagctgtcttggctttgatgtcccttctctgcgttgtttaacatc	4956
Qy	5262	aagggcattcgacacatgctcttcgcgttgccatgtgcgtgcgcgcctgtttcaacatc	5321
Db	4957	ggcctctgcttcttctgggtcatgttcaatcctagcgaatctttggaatgtcccaacttgc	5016
Qy	5322	tgcctgctgctgttctcttgctcatgttcattcttgccattttcggcagtcgtgtcttcag	5381
Db	5017	tatgtataaagggaagatgggaatlaatgacatgttcaattttgagaccctttggcaacagt	5076
Qy	5382	cacgtgaaaggaaagacggcgcatcancgacgtctacaacttcaagaccttgccagac	5441
Db	5077	atgatttgctgttcccaataccaacctctgctggctgggatggtctagcaactatt	5136
Qy	5442	atgatcctgctcttttcagattgctacgtgacccggttggatgggtgacgtggacggcatt	5501
Db	5137	cttaacagtaagccaccgactgagcccaaaaagtctcatctggaagtccaattgaa	5196
Qy	5502	atcaattgaaagacatgcga-tcc-accgcagac-ga-caaag-gcta--tccg-g--	5550
Db	5197	ggagactggttaaccatctgttggaaatactactttgttagttatcatcatatcc	5256
Qy	5551	gca-attgtggttcagcgaccgttggaataacggtttcctctcataccagttataagc	5609
Db	5257	ttcctggttgtgaacatgacattcagtcacactggagaattttagttggcaact	5316
Qy	5610	tttttgatagttaattaatatgatactgctcatctcgagaaactatgtagccacc	5669
Db	5317	gaagaagtagtgaacctgagtgagtgactttgagatgttctatgaggtttggag	5376
Qy	5670	gaggactgcgaagggtctaacccgacgacactacgacatgtactatgagatctggcag	5729
Db	5377	aagttgatcccgatcgagccagtttatagagttctcaaacctctgatttgcagct	5436
Qy	5730	caatttcgatccggaggccaccagtagtacaatccgtatgacgtgtcggatttcttgac	5789
Db	5437	gacctgatctctctcttctcatagcaaaacccaagaatccagctcattgccaatgat	5496
Qy	5790	gtactggagcccgctgcagatccacaaacgacaagatcaagatcatatcatgatgac	5849
Db	5497	ctgcgccatggttagtggagccggaatccattgtcttgacatcttattgtctttacaaa	5555
Qy	5850	ataccatctctgcggtgacctcattgtacttgcgtgcgacatcctcgacgcctttacga	5908

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RESULT      8
ID T30195 standard; cDNA; 6404 BP.
AC T30195;
DE 25-OCT-1996 (first entry)
DE peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
DE Human; peripheral nervous system; sodium channel; PNIB;
KW dorsal root ganglion; sodium-agonist; sodium-antagonist;
KW drug screening; analgesic; hypotensive; antiinflammatory; trauma;
KW pain; neurological disorder; antisense; gene therapy; ss.
OS Homo sapiens.
FH      Location/Qualifiers
FH key      49..5015
FH cds
FT FT      /*tag= a
FT FT      /product= PNIB protein
FT FT      misc_difference 334..336
FT FT      /*tag= b
FT FT      /codon= seq:ACA, aa:Ala
FT FT      misc_difference 1738..1740
FT FT      /*tag= c
FT FT      /codon= seq:ATA, aa:Leu
FT FT
FT FT      W09614077-Al.
FT FT      17-MAY-1996.
PD PF      02-NOV-1995; U14251.

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02-NOV-1994; US-334029.  
07-JUN-1995; US-482401.  
PR (TROP-) TROPHIX PHARM INC.  
PA (UINY ) UNIV NEW YORK STATE RES FOUND.  
PI Borden LA, Halegoua S, Mandel G;  
WP1: 96-251547/25.  
DR P-PSDB; R93641.  
PT Nucleic acid encoding peripheral nervous system specific sodium  
channel peptide - useful for sodium channel-associated disease or  
trauma.

Example 4; Fig 14; 80pp; English.  
The sequence encodes a human peripheral nervous system sodium channel  
peptide-l alpha-subunit (PNLB), with sodium channel activity. A  
probe has been isolated by PCR from a human peripheral nervous  
system cDNA library, using probes derived from the rat PNL protein  
sequence (R93638-39), and has been used to screen a human dorsal  
root ganglion cDNA library, to give the full-length sequence, using  
PCR primers T30198-99 and T18167. A related sequence (T30194) has  
also been isolated. The sodium channel peptide may be used to  
isolate sodium-agonists and sodium-antagonists for use as  
analgesics, hypotensives, antiinflammatories, and in therapy of  
sodium channel-associated pathology or trauma, e.g. neurological  
disorders. The DNA (in sense or antisense orientation) may be used  
in gene therapy.

Sequence 6404 BP; 1961 A; 1236 C; 1381 G; 1926 T;

Query Match 4.7%; Score 308; DB 22; Length 6404;  
Best Local Similarity 62.2%; Pred. No. 7.08e-190;  
Matches 1231; Conservative 0; Mismatches 713; Indels 35; Gaps 25;

D Db 3614 ttgaacacagttgttggaaagtctattgtcctcatgatccctgcctcagcagtggtgcc 3673

Q Y 3961 TTGAAAATAAATATTTTGAAACAGCTGTATCAATCATATGATTTTAATAGTAGTGCTTAGCTT 4020

D Db 3674 tggctttgaagatatattatattaagaaggaaaaaccataagattactctcgagtcgtg 3733

Q Y 4021 TGCGCATTAGAAGATGCATCTGCCCAAAGACCCTACTGTCAGGATATTTTACTACTATA 4080

D Db 3734 cagacaagatcttcacctcacattcttctcgtggaaaagtcctcaaatggatgcatgatg 3793

Q Y 4081 TGGCACAGATATTATTACGGTTATATTCTTCTTGGAAATGTTTAATCAAGTGGTGGCGGCTG 4140

D Db 3794 gttataaacacatttoaccaatgcttgtttggctggattctcctaattggtgatgtt 3853

Q Y 4141 GCTTCAAAGTGATGTCTCCAACACGGTGGTGTGGCTCGATTCGTGATTGTCATGTFAT 4200

D Db 3854 ctttggttacttagtggcaaacactcttggctactcagatcttggcccccaattaaatccc 3913

Q Y 4201 CGCTTATCAACTTCGTTGCTTCACATTGTGGAGCGTGGTGGTATTCAAGCCTTCAAGACTA 4260

D Db 3914 ttggcacactgagagctttaagacctctaagagccttatctagatttgaaagaatgaggg 3973

Q Y 4261 TGCCAACGTTAAGAGCAGCTGAGACCACACTACGTGCCATGTCCCGTATGAGGGCAGTAGGG 4320

D Db 3974 tcgtttgaatgcactcattagagcaaattccttcctcatcataatgtctacttgggtgtc 4033

Q Y 4321 TCGTGCTGAATGGCTGGTGCACAGCTATACCGTCCATCTTCAATGTGCTATTGGGTGTGC 4380

D Db 4034 ttatattctggctgatatttcagcatcatgvggagtaaaattgttttgcctcggcaagttcctatg 4093

Q Y 4381 TAATATTTTTGGCTAAATTTTGGCCATAATGGGTGTACAGCTTTTGTCTGGAAAAATATTTTA 4440

D Db 4094 agtgattaaacacacagatgggttcacggttttcctgcgaagtcgaagtccaatcttcctcg 4153

Q Y 4441 AGTTCGGAGGACATGAATGGCACCA-A-GUTCACCCAGCAGATCA-TACCANAATCG--C- 4493

D Db 4154 aatgttttggccttatgaatgttagtcaaaatgtgcgatggyaaaaacctgaaagtgaact 4213

Q Y 4494 AATGCCCT-GCG---A-GAGCGAGAA-CTACACGTGGG-TG---AATTTCAGCAA-TGAATT 4542

D Db 4214 ttgataatgtgcgacttggttacctatctctgcttcaagtgcacattgaaccttttaaggatgga 4273

Q Y 4543 TCGATCATGTAGSPAACCGCTATCTGTGCCCTTTTCCAAAGTGGCCACTTCCAAAGGCTGGA 4602

Db	4274	cgattattatgtgcagcagtgattctgtttaaagttagacaagcagccaaatatgaat	4333
Qy	4603	TACAAATCATGAACAGTGTATCGAATTCAGAGAGGTGGACACGACCAATTCGTGAAA	4662
Db	4334	atagccctcacatgtattatttttttggctgtgttattcatcttttgggtcatcttcttcaact	4393
Qy	4663	CGAACATCTACATGTATTTATATTTTCGTATTCTTCATCATATTTGGATTCCTTTTTCACAC	4722
Db	4394	tgaacttgcttcattgggtcatcatagataaatttcaaccacacagaa-aaagaagcttggga	4452
Qy	4723	TCAATCTGTTTCATTTGTTTATTCATTTGATATTTTAATGACCAAAAGAAAAGAGAGTG	4782
Db	4453	gggtca--agacatctttatgcagagaacagagaagaataactataatgcataaagcaaaagc	4510
Qy	4783	GATCATTAAGAATGTTTCATGCAGAGAAGATCAGAAAAGTACTATAATGCTATGA AAAAG	4842
Db	4511	tgggggtccaaagaagccaaaaagccaatcttcgaccagggaacaaatccaaggtatgta	4570
Qy	4843	TGGGCTCTAAAAAACCAITTAAGGCCATTCACAGACCANGTGGCGACCAACAGCAATAG	4902
Db	4571	tatttgacctagtgcacaatcaagcctttgatatttagtatactatggttcttctatctgtcca	4630
Qy	4903	TCCTTTGAAATAGTAAACCATAGAAATTCGAATAATCATTTATGTTTATTCATTGGTCTCGA	4962
Db	4631	acatggttaaccatgatggtagaaaaagagggt- caaagtccaacatagtactgaagtttca	4689
Qy	4963	ACATGTTCCACATGACCCTCGATCGTTACGATGCGTCCGACGCTATAAC- GCGGTCTTA	5021
Db	4690	tattggataaatgtgggttttataatccctttcactggagaatgtgtctaaactgctc	4749
Qy	5022	GACTATCTCAATGGCATATTCGTAGTTATTTTCAGTTCCGAATGCTATTAAAAATATTC	5081
Db	4750	tccttcagacactactcactcactgtaggatggaataattttgattttgtgtgtgtgatt	4809
Qy	5082	GCTTTACGATATCACTATTTTATTGACCCATGGAAATTTATTGATGATAGTACTGTCTATT	5141
Db	4810	atctccatgttagtattgttcttagctgatttgattgaaacgtattttgtgtccctcacc	4869
Qy	5142	TTATCCATCTTAGTCTGTACTTAGCGATATATTGAGAAAGTACTTCGTGTCCGCGACC	5201
Db	4870	ctgttccagtgatccgtcttgcaggattggccgaatcctcagctctagtcaaaaggagca	4929
Qy	5202	CTGCTCCGAGTGTGCGTGTGGCGAAGTGGGCGGTGTCTTCGACTGGTGAAGGGAGCC	5261
Db	4930	aagggatccgcacgctgctcttgtttgttagtgcctcctcctgcgtgttttaacatc	4989
Qy	5262	AAGGCGATTCGGACACTGCTCTTCGGGTGGCCATGTCCTCCCGGCCCTGTTCAACATC	5321
Db	4990	ggcctcctgctcttcctggctcatgttcatacgaacatcttggaaatgtccaaactttgcc	5049
Qy	5322	TGCTGTGCTGTCTTCCTGGTTCATGTTCACTTTTGCCATTTTCGGCATGTCGTTCTTCATG	5381
Db	5050	tatgttaaaagggaagatggaataatgatcatgttcaattttggacacctttggcaacagt	5109
Qy	5382	CACGTGAAGGAGAAGAGCGCATTAACGAGCTACACTTCAAGACCTTTGGCCGAGC	5441
Db	5110	atgatttgcctgttccaaattacaacctgtgtggtggatgtgactgtagcacctatt	5169
Qy	5442	ATGATCTGCTCTTTTCAGATGTGCGAGTCCAGCGGTGGATGGTGTACTGGACGCCATT	5501
Db	5170	cttaacagtaagccaccgactgtgacccaaaaaagtctactcctggaagtcaagtgtgaa	5229
Qy	5502	ATCAATGAGGAAGCATGCGA-TCC-ACCGACAGC-GA-CAAAG-GCTA--TCGG--G--	5550
Db	5230	ggagactgtgtgaaccatctgttggaaatatcttacttctttagttattatacatcatcc	5289
Qy	5551	GCA-ATGTGGTTTCAGCGACCGGTGGAAATACGTTTCTCCTCTCATACCTAGTATAAGC	5609
Db	5290	ttcctggttgggtgaacatgtacattgcaatcatactggaagatttagtgttgcacat	5349
Qy	5610	TTTTTGATGTTATTAATGATGATGATGCTGCTATCTTCGAGAAGTACTAGTACGGCCAC	5669

Db 5350 gaagaaagtactgaacctctcgtgaggtgagtgactttgagattctcattgaggtttggggag 5409  
 QY 5670 GAGGACGTGCAAGAGGGTCTTAACCGACGACTACGATCTACTGATCTGAGATCTGGCAG 5729  
 Db 5410 aagttgatcccgatcgagcccgattatagagttctctaaactctctgattttcagct 5469  
 QY 5730 CAAATCGATCCGGAGGGCACCCAGTACATACGCTATGATCAGCTGTGCCAAATTCCTGGAC 5789  
 Db 5470 gccctggatctctcttctcatagcaaaacccaacaaagtcacgtccagctcattgcatgat 5529  
 QY 5790 GTACTGGAGCCCGCTGCAGATCCCAACACCGACAAAGTACAAGATCATATCGATGGAC 5849  
 Db 5530 ctgccatggttagtggtgacggatccattgtcttgacatcttattgcttttcaaa 5588  
 QY 5850 ATACCATCTGTGCGGGTGACCTCATGTACTGCTCGACATCTCTGACGCCCTTACGAA 5908

RESULT 9  
 ID T77803 standard; cDNA; 6524 BP.  
 AC DT T77803;  
 DE DT 09-OCT-1997 (first entry)  
 DE DE CDNA encoding wild type rat DRG (SNS-B).  
 KW Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;  
 KW modulator; impulse; sensory neuron; acute pain; chronic pain;  
 KW neuropathic pain; glia; muscle; parasympathetic nervous system;  
 KW enteric nervous system; central nervous system; dorsal root ganglia;  
 KW cranial ganglia; ss.  
 OS Rattus rattus.  
 FH Key Location/Qualifiers  
 FT Cds 204..6077  
 FT /\*tag= a  
 FT /product= Rat\_DRG(SNS-B)  
 PW WO9701577-A1.  
 PF 16-JUN-1997.  
 PR 25-JUN-1996; G01523  
 PR 28-JUN-1995; GB-013180.  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 PI Akopian AN, Wood JN;  
 DR WPI: 97-100165/09.  
 DR P-PSDB; W21737.  
 PT New isolated mammalian sensory neuron sodium channel protein - used  
 PT to identify modulators of the sodium channel, partic. for the  
 PT treatment of pain  
 PS Claim 9; Page 50-58; 128pp; English.  
 CC The sequences given in T77803-06 encode the wild type and three  
 CC variant forms of a rat sensory neuron sodium channel protein which  
 CC is insensitive to tetrodotoxin. The proteins can be used for  
 CC identifying modulators of the sodium channel. Blockers of the  
 CC sodium channel will block or prevent the transmission of impulses  
 CC along sensory neurons and thereby be useful in the treatment of acute,  
 CC chronic or neuropathic pain. The novel protein is found only in sensory  
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,  
 CC enteric or central nervous system. The protein is found preferably in  
 CC the neurons of the dorsal root ganglia or cranial ganglia.  
 SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T;

Query Match 4.58; Score 296; DB 32; Length 6524;  
 Best Local Similarity 63.88; Pred. No. 2,37e-181;  
 Matches 890; Conservative 0; Mismatches 486; Indels 18; Gaps 11;

Db 4254 aacttcgacaacgtcgctatgggctaccctcgcaactcttcagggtgcaacctcaaggc 4313  
 QY 4539 AATTTCGATCATGTAGTAACGGTATCTGTCCCTTCAGTGGCCACCTTCAAGGC 4598  
 Db 4314 tggatggacataatgatcagctgttattccggagagatacaacagtcagcttaactgg 4373  
 QY 4599 TGGATACAATCATGAAACGATGCTATCGAATTCACGAGAGGTGGAAGCAACCAATTCGT 4658  
 Db 4374 gagacaacattgtacatgtacctgtacttcgtcttcattcatcttcggtgcctcttc 4433  
 QY 4659 GAAACGAACATCTACATGATTTATATTCGTATCTTCAATCATATTTGGATCCTTTTC 4718  
 Db 4434 agcgtgaactctttgttgggggtcaatactgcacaacttcaaccacagaaaaaagcta 4493

[illegible]









12-MAY-1995 (first entry)  
scd61, a subclone of hscpl, encodes a non-dipteran sodium channel.  
non-dipteran sodium channel; lepidoptera; insecticide; sensitivity;  
target site; pyrethroids; marker; resistance; probes; detection;  
sense primer; PCR; polymerase chain reaction; Heliothis; degenerate;  
Drosophila melanogaster; homologue; hscpl; para locus; scd61; ss.  
Heliothis virescens.

OS Location/Qualifiers  
Key 297  
intron FT /\*tag= a  
FT /note= "end of intron"  
FT 298..441  
FT exon FT /\*tag= b  
FT complement (319..338)  
FT primer\_bind FT /\*tag= c  
FT /note= "HSC 3455+ ('abelard') (numbering based on  
the Drosophila homologue 'para')"  
FT intron FT 440..522  
FT /\*tag= d  
FT exon FT 523..795  
FT /\*tag= e  
FT intron FT 796..882  
FT /\*tag= f  
FT exon FT 883..1055  
FT /\*tag= g  
FT intron FT 1056  
FT /\*tag= h  
FT /note= "start of intron"

CA2112445-A.  
PD 01-JUL-1994.  
PF 24-DEC-1993; 112445  
PR 30-DEC-1992; US-998289.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PI Black BC, Kreitman M, Taylor M;  
WPI: 94-272316/34.  
DR P-PDSB; R60495.  
PT Gene fragment encoding a non-dipteran sodium channel - for  
detecting insecticide sensitivity or resistance in insects, pref.  
PT Lepidopterans  
PS Example 2; Fig 1; 32pp; English.  
SC Q71200-202 are the DNA sequences of the subclones, scd61, scd72, and  
scd131 respectively, from the genomic clone "hscpl". The hscpl clone is  
approximately 8000 bp and encodes a sodium channel protein. The  
clone was isolated from a Pyrethroid resistant PEG-87 library. The  
non-dipteran sodium channel is thought to be the target site for  
sensitivity to a variety of different insecticides and is useful as a  
marker for target insensitive insecticide resistance. Q71198-99 are  
degenerate primers used to isolate hscpl. The primers are based on an  
homologous sequence of the Drosophila para locus, in particular a  
portion of an exon in the fourth transmembrane domain of the a-subunit.  
SQ Sequence 2416 BP; 709 A; 436 C; 487 G; 756 T;

Query Watch 1.5%; Score 96; DB 12; Length 2416;  
Best Local Similarity 77.0%; Pred. No. 1.14e-42;  
Matches 137; Conservative 0; Mismatches 41; Indels 0; Gaps 0

Dbb 882 ggctttgaagatgtcaattaccacacacgacgattcttcacgatattgcacttgccttg 941  
|||||  
Qyb 4022 GGCAATTAGGAATGTACATCTGCCAACAAACCACCATCTGCGAGGATAATTTTACTATAT 4081  
|||||

Dbb 942 ggcacggatcttcacccgcatcttcttcacgatgttgtacaaatggcttgccttg 1001  
|||||

Qyb 4082 GGACGAATATTTCACGGTTATTCTCTTGGAAATGTAATCAAGTGCTGGCGCTCG 4141  
|||||

Dbb 1002 ctcccgagaatacttcacaaaatcgctggctggctgcagacttcattgctcatgta 1059  
|||||

Qyb 4142 CTTCAAAGTGACTTCACCAACGGGTGGTGTGGCTCGATTCGTGATGTCATGTA 4199  
|||||

RESULT 15  
ID N81164 standard; DNA; 204 BP.  
AC N81164;  
DT 08-NOV-1990 (first entry)

```

DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key
FT Location/Qualifiers
FT misc_feature 19..69
FT /tag= a
FT /function-multiple cloning site
FT primer_bind 187..204
FT /tag= b
FT
FN EP-285123-A.
PD 05-MAY-1988.
PF 30-MAR-1988; 105163.
PR 03-APR-1987; US-034819.
PA (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
DR WPI; 88-279927/40.
PT Introducing random point mutations into nucleic acids -
PT by prepn of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure; P; English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
Query Match 0.8%; Score 50; DB 1; Length 204;
Best Local Similarity 17.2%; Pred. No. 1.25e-13;
Matches 21; Conservative 63; Mismatches 36; Indels 2; Gaps 2;
Db 78 dchvgccgymrttt-hhyrrmrbnvrydnrsdaawyc-cyrsvkydcynachddh 135
QY 5722 TCCTGGAGCAATTCGATCCGGAGGCCGCCAGTACATACGCTATGATGCTGCCGAAT 5781
Db 136 yvybbvynvnhnncnccbnhvnbnhrnwayvrhdarrddvhccvchccgat 195
QY 5782 TCCTGGAGCTACTGGAGCCCCCGCTCGAGATCCCAACCCGACAGTACAAGATCATAT 5841
Db 196 cg 197
QY 5842 CG 5843

```

Search completed: Wed Jul 8 01:38:48 1998  
 Job time : 1620 secs.

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\*\*\*\*\*  
 W A P E S R E L E A S E  
 \*\*\*\*\*  
 (TM)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
 Run on: Tue Jul 7 22:17:15 1998; MasPar time 7009.21 Seconds  
 Tabular output not generated.

Title: >US-08-554-424-7  
 Description: (1-6513) from US08554424.seq  
 Perfect Score: 6513  
 N.A. Sequence: 1 TCTAGACGTTGGCCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513  
 Comp: AGATCTGCAACCGCGGTATC.....TGGCTCATATGAGATCT

Scoring table: TABLE default  
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1759237 seqs, 667866413 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: emb1-est54  
 1'em\_est1 2'em\_est3

Database: genbank-est106  
 3:gb\_est1 4:gb\_est10 5:gb\_est11 6:gb\_est12 7:gb\_est13  
 8:gb\_est14 9:gb\_est15 10:gb\_est16 11:gb\_est17  
 12:gb\_est18 13:gb\_est19 14:gb\_est20 15:gb\_est21  
 16:gb\_est22 17:gb\_est23 18:gb\_est3 19:gb\_est4 20:gb\_est5  
 21:gb\_est6 22:gb\_est7 23:gb\_est8 24:gb\_est9 25:gb\_gss  
 26:gb\_sts

Statistics: Mean 12.783; Variance 2.249; scale 5.685

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	124	1.9	343	20	HSC2HD061 H. sapiens partial cDN	2.56e-199
2	121	1.9	529	23	ms53e02.r1 Life Tech m	1.13e-192
3	99	1.5	594	24	AA272867 vb09f10.r1 Soares mous	1.36e-144
4	91	1.4	619	25	F.rubripes GSS sequenc	1.85e-127
5	77	1.2	413	10	AA272673 ve83f11.r1 Soares mous	4.40e-98
6	70	1.1	252	13	AA754459 97SN1787 Rice Immature	9.27e-84
7	62	1.0	214	4	AA360938 EST70140 T-cell lympho	8.97e-68
8	64	1.0	252	13	AA754459 97SN1787 Rice Immature	1.00e-71
9	65	1.0	573	11	AA699257 HL08049.5prime HL Dros	1.03e-73
10	59	0.9	247	13	AA754458 97SN1784 Rice Immature	6.62e-62
11	60	0.9	247	13	AA754458 97SN1784 Rice Immature	7.47e-64
12	49	0.8	435	16	AA885211 am34c11.s1 Soares NFL	5.67e-43
13	50	0.8	437	25	FR0002729 F.rubripes GSS sequenc	8.14e-45

14	0.7	225	16	AA214661	zq89e09.r1 Stratagene	3.33e-32
15	0.7	386	25	FR0002750	F.rubripes GSS sequenc	9.81e-36
16	0.7	407	25	FR0002732	F.rubripes GSS sequenc	9.81e-36
17	0.7	604	25	FR0002761	F.rubripes GSS sequenc	9.81e-36
18	0.7	619	25	FR0002759	F.rubripes GSS sequenc	9.81e-36
19	0.6	267	10	AA620400	ae57d03.s1 Stratagene	4.91e-27
20	0.6	407	25	FR0002725	F.rubripes GSS sequenc	1.83e-30
21	0.6	499	7	AA446878	zw90c04.s1 Soares tota	4.91e-27
22	0.6	546	7	AA446997	zw90c04.r1 Soares tota	2.04e-20
23	0.6	619	25	FR0002754	F.rubripes GSS sequenc	1.83e-30
24	0.6	2275	12	AF034173	Homo sapiens ntcon2 co	2.04e-20
25	0.5	163	13	AA798309	ub61c07.r1 Soares mous	8.09e-19
26	0.5	267	5	AA383040	EST96341 Testis I Homo	3.03e-17
27	0.5	269	16	AA867902	TENS0009 T. cruzi epim	3.03e-17
28	0.5	271	26	G16013	human STS CHLC.GCT13C0	3.03e-17
29	0.5	355	21	HSZ78350	H.sapiens mRNA, expres	1.07e-15
30	0.5	374	23	AA144007	mr75b01.r1 Stratagene	3.03e-17
31	0.5	384	12	AA112441	zm27g02.r1 Stratagene	8.09e-19
32	0.5	405	24	AA065344	b0250t1 Testis 5 Homo	1.07e-15
33	0.5	409	23	AA153254	mr77c01.r1 Stratagene	3.03e-17
34	0.5	413	4	AA306559	EST177527 Jurkat T-cel	8.09e-19
35	0.5	419	20	HSDECO59	H. sapiens partial cDN	3.03e-17
36	0.5	437	25	FR0002733	F.rubripes GSS sequenc	3.03e-17
37	0.5	443	21	HSZ78389	H.sapiens mRNA, expres	1.07e-15
38	0.5	467	12	AA705382	zj99h09.s1 Soares feta	1.07e-15
39	0.5	532	7	AA445889	SWAMCA1728SK Bruglia ma	3.03e-17
40	0.5	559	26	G16023	human STS CHLC.GCT14F0	1.07e-15
41	0.5	650	20	W27487	31g4 Human retina cDNA	8.09e-19
42	0.5	736	11	AA567426	HL01171.5prime HL Dros	3.03e-17
43	0.5	770	26	AF021116	Homo sapiens trinucleo	1.07e-15
44	0.5	2275	12	AF034173	Homo sapiens ntcon2 co	1.07e-15

## ALIGNMENTS

RESULT	LOCUS	1	HSC2HD061	343 bp	RNA	EST	21-SEP-1995
DEFINITION			H. sapiens partial cDNA sequence; clone c-2hd06, mRNA sequence.				
ACCESSION			F07776				
NID			G677276				
KEYWORDS			EST; partial cDNA sequence; transcribed sequence fragment.				
SOURCE			Homo sapiens				
ORGANISM			Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE			1 (bases 1 to 343)				
AUTHORS			Genexpress.				
TITLE			Direct Submission				
JOURNAL			Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France				
REFERENCE			2 (bases 1 to 343)				
AUTHORS			Genexpress.				
TITLE			The Genexpress cDNA program				
JOURNAL			Unpublished				
REFERENCE			3 (bases 1 to 343)				
AUTHORS			Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Poullot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.				
TITLE			IMAGE: molecular integration of the analysis of the human genome and its expression				
JOURNAL			C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)				
MEDLINE			95277534				
COMMENT			Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector; Sequencing_method: single read, full automatic; Primer: M13_reverse cDNA sequence colinear to mRNA Stretch_removed: nothing Normalization_method: Bento Soares, P.N.A.S. 91:9228:9332(1994);				

Wed Jul 8 10:17:03 1998

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Genexpress_library_id: C;
Genexpress_sequence_id: ylc-2hd06.
FEATURES
    source
        1..343
            Location/Qualifiers
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## FEATURES

BASE COUNT	ORIGIN
68 a	5 others

BASE COUNT	68 a	78 c	80 g	112 t	5 others
BASE COUNT	68 a	78 c	80 g	112 t	5 others

Query Match	1.98;	Score 124;	DB 20;	Length 343;
Best Local Similarity	67.3%;	Pred. No. 2.56e-199;		
Matches	231;	Conservative	0;	Mismatches 112; Indels 0; Gaps 0;
Db	1	TTCTCTCCATGTAGGAATGTTTCCTGGCTCAACTGATAGAAAAAGTATTTTGTGTGCCCTA	60	
Qy	5140	TTTATTCACATCTTAGGTCTGTACTTAGCGATATATCGAGAGTACTTCTGTTCGCCGA	5199	
Db	61	CCCTGTTTNCAGTAGTATCCGCTTTCGCCAGGATGSCCGAATCCTACGCTCTGATCAAAAGG	120	
Qy	5200	CCCTGCTCCGAGTGGTGGCTGTCGCGAAAGTGGSCCGCTCTCTTCGACTGGTGAAGGGAG	5259	
Db	121	CAAAAGGGATCCGCACCGTGTCTTTGCTTGTATGATGTCCCTTCCTGCGTTGTTTAAACA	180	
Qy	5260	CCAAAGGGCATTTCCGACACTGTCTTCGCGTTGGCCATCTCGCTGCCGCCCTGTTTCAACA	5319	
Db	181	TCGGNCTCCTTCTTTTCTCGTGTCAATGTTCACTACGNCATCTTTGGGATGTCCAAATTTTG	240	
Qy	5320	TCTGCTCTGCTGTCTTCTCGTGTCAATGTTCACTTTGGCATTTTCGGCATGTCTCTTCA	5379	
Db	241	CCTATGTTTAAAGGGAAGTGTGGGATCGATGACATGTTTNNCTTTTGAGACCTTTTGGCAACA	300	
Qy	5380	TGCAGTGAAGGAGAAGCGGCATTAACGACGCTCTACAACCTTCAAGACCTTTTGGCCAGA	5439	
Db	301	GCATGATCTGCTGTGTTCCAAATTAACAACCTCTGCTGGCTGGGA	343	
Oy	5440	GCATGATCTGCTGTCTTTTCAGATGTTCGAGCTCAGCGGTGTGGGA	5482	

RESULT	2	AA183990	529 bp	mrna	EST	07-JAN-1997
LOCUS		ms3502.r1	Life Tech mouse embryo	13 54pc	10666014	Mus musculus
DEFINITION		cdna clone 615290 5'	similar to gb:M81758 SODIUM CHANNEL PROTEIN			
			SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:02707 Mus musculus			
			voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mrna			
			sequence.			

ACCESSION	AJ183990
NID	91767357
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 529) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and AUTHORS

TITLE	COMMENT
The WashU-HHMI Mouse EST Project Unpublished (1996)	Contact: Marra M/Mouse EST project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800

Fax: 314 286 1810  
Email: mousest@wustl.edu  
This clone is available royalty free through LLNL ; contact the  
IMAGC Consortium (info@image.llnl.gov) for further information.  
MGI:376114  
Seq primer: -28M13 rev1 from Amersham  
High quality sequence stop: 263.

## FEATURES

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1. 529
/organism="Mus musculus"
/strain="C57BL/6J"
/note="vector: pcwMv-SP0RT2; Site_1: SalI; Site_2: NotI;
Cloned unidirectionally. Primer: Oligo dT. 13.5dpc
embryos. pcwMv-SP0RT2 vector."
/db_xref="taxon:10090"
/clone="615290"
/clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
/dev_stage="13.5dpc embryos"
/lab_host="DHI0B"
<1. .>529
96 a 169 c 121 g 143 t
mRNA
BASE COUNT
ORIGIN

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Query Match	1.9%	Score 121:	DB 23:	Length 529:
Best Local Similarity	70.1%:	Pred. No. 1.13e-192:		
Matches 220:	Conservative 0:	Mismatches 93:	Indels 1:	Gaps 1:
Db	190	TCGCCAGCGTCTTACGCGTCATCCGCTCGCCAGAGATCGCGCGCATCCTCAGCGCTGATT	249	
Qy	5193	TTCGGGACCCCTGCTCCGAGTGGCTGCTGGCGAAGCTGGCCGTGTCCTTCGACTGGTG	5252	
Db	250	CGAGCAGCCAAAGGGGATTCGACGCTGCTTTGCGCCCTCATGATGTCCTTCGCCGGCCCTC	309	
Qy	5253	AAGGAGCCAAAGGCAATTCCGACACTGCTCTCGCTTGCCCATGTCGCTCGCGGCCGTG	5312	
Db	310	TTCAACATCGGCCCTCCTCCTTCCTCGTCATGTTCACTACCTCCATCTTCGCGCATGGCA	369	
Qy	5313	TTCAACATCTGCCCTGCTGCTGTTCCGTGTCATGTTTCATCTTTGCCAATTTTCGGCATGTCG	5372	
Db	370	G-CTTCGCTATGTCATAGATGAGGCTTGGCATGCACGACATGTTCAACTTCAAGACCTTT	428	
Qy	5373	TTCTTTTCATGCACTGAGGAGAAAGGGCAATTACGACGCTTACACTTTCAGACCTTT	5432	
Db	429	GGCAACACGATGCTGTGCTTTTTCAGATACCACGCTCGGCTGGCTGGGATGGCCCTCCTC	488	
Qy	5433	GGCCAGAGCATGATCCTGCTCTTTCAGATGTGCAGCTCAGCGCGTGGGATGGTGTACTG	5492	
Db	489	AGCCCCATCCTCAA	502	
Qy	5493	GACGCCATTACAA	5506	

3	RESULT	AA272867	594 bp	mRNA	EST	26-MAR-1997
	LOCUS	vb09f10.r1	Soares mouse NML	Mus musculus	cDNA clone	748459.5
	DEFINITION	similar to gb:M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mRNA sequence.				
	ACCESSION	AA272867				
	NID	g1907742				
	KEYWORDS	EST.				
	SOURCE	house mouse.				
	ORGANISM	Mus musculus				
		Eukaryotae; mitochondria				
		Eukaryotae; Chordata;				
		Vertebrata; Eutheria;				
		Rodentia; Sciurognathi;				
		Muridae; Murinae;				
		Mus.				
	REFERENCE	1 (bases 1 to 594)				
	AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geiseli,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
	TITLE	The WashU-HMHI Mouse EST Project				





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Pr: M13 Reverse Primer.
Location/Qualifiers
1..252
/organism="Oryza sativa"
/cultivar="Milvanc23"
//note=Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZAP11
vector at 5'end with EcoRI and 3' end with Xho I site."

```

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O.gammasm="Olya sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript
XhoI; Directional CDNA library
vector at 5' end with EcoRI
/db_xref="taxon:4530"
/clone="97SN1787"
/clone_lib="Rice Immature Seed"
/tissue_type="Immature Seed"
/dev_stage="5 days after poll"
/lab_host="E. coli SOLR"

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BASE COUNT 3 a 21 C 12 g 33 L 179 OLNEIS  
ORIGIN

Query Match 1.08; Score 64; DB 13; Length 252;  
Best Local Similarity 11.68; Pred. No. 1.00e-71;  
Matches 26; Conservative 115; Mismatches 82; Indels 2; Gaps 2;

303 CCGGCGGATTTGGCCCTCCACACCTCTCGAGGATATGATCCCCCTACTACACCAATGACTG 392  
QY  
82 VBNTKVDVGNHTRCSRWBRVTRMAHYHDYTCBYYNNNDYHMHHBMYBBTGCMTCTMMC 141  
Db  
363 ACATTGGTAGTCTTAAGCAAGGAAAGATATTTCGTCTTTCTGCATCAAAAGCAATG 422  
QY

Db	142	WBHYNTKCTASGWHHTSTNYDVKSTNTGWTSYSDKSMHGVCWSBBYKXHKVSTTRATR	201
QY	423	TGG-ATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTACATTCT-AGTGCA	480
Db	202	SYTCVRKYCYMNTTKVVKYKHVVHBGCGHETDSCKTMMNTMNHV	246
QY	481	CAITATTTCCTTCATCATCATCACCAATTCCTCGTCAACTGCA	525

ACCESSION	AA095237
NID	92702186
KEYWORDS	EST.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster

REFERENCE  
1 (bases 1 to 573)  
Drosophilidae; Drosophila.  
Pterygota; Diptera; brachycera; Muscomorpha; Ephydrogata;  
Drosophilidae; Drosophila.  
AUTHORS  
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,  
Brokstein, P., Lewis, S. and Rubin, G.M.  
BDGP/HHMI Drosophila EST Project  
TITLE  
Unpublished (1997)  
JOURNAL

CONFERENCE (1997)

CONTACT: HARVEY, D.  
G. M. RUBIN-MOLECULAR AND CELL BIOLOGY  
UNIVERSITY OF CALIFORNIA BERKELEY  
539 LSA, BERKELEY, CA 94720-3200, USA  
Fax: 510 643 9947

```

FEATURES
source
1. .573
Location/Qualifiers
High quality sequence stop: 426.
plate: 80 row: E column: 1
High quality sequence stop: 426.
Location/Qualifiers
1. .573
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"/note="Organ: embryo; Vector: pOT2; Site_1: ECORI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2."
/db_xref="taxon:7227"

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/clone="HL08049"
/clone_lib="HL Drosophila melanogaster head pot2"
/sex="male and female"
/dev_stage="head-brain & sensory organ"
/lab_host="XLI Blue"

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BASE COUNT	129 a	147 c	145 g	152 t	ORIGIN
Query Match	1.08;	Score 65;	DB 11;	Length 573;	
Best Local Similarity	62.9%;	Pred. No. 1.03e-73;			
Matches	171;	Conservative	0;	Mismatches 100;	Indels 1; Gaps 1;
Db	23	GGCGGTATATGCGGTGATCAAGGCCGCCAAGGGGATCAGAAGTTCGTATTTCGCTCTC	82		
QY	5232	GGCCGTGTCTCTTCGACTGTGTGAAGGGAGCCAAAGGGCATTCGGACACTGCTTCCTCGCGTTG	5291		
Db	83	GTAGTGTCCCTGTCGCCGCCCTATTAAACATCGGAGCTCTGCTAGGACTGATCACCTTTATC	142		
QY	5292	GCCATGTGCGTGGCGGCCCTGTTCAACATCTGCGCTGCTGCTCTTCCTGGTCATGTCATC	5351		
Db	143	TACGCAATTCCTGGCGATGTCGCTGTTTCGGAAATGTCAAGCTCCCAAGTGCTCTCGAGAC	202		
QY	5352	TTTGGCCATTTTCGGCATGTGCTTCTTCATGACGTGAAGGAGAGCGGCATTAAACGAC	5411		
Db	203	ATGGTGAACCTTCAGACACTTCGGGCGCA-CATGCACTTACTGTCGGTGTGATGACCTCA	261		
QY	5412	GTCTACAACTTCAGACCTTTGGCCAGAGCATGATCGCTCTTTTCAGATGTCGACGTCA	5471		
Db	262	GCCGGGTGGAATGACGCTACTTGGTCCCTGAT	293		
QY	5472	GCCGGTTGGATGGTGTACTGAGCGCATTAT	5503		

<b>RESULT</b>	10				
<b>LOCUS</b>	AA754458	247 bp	mRNA	EST	20-JAN-1998
<b>DEFINITION</b>	97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.				

ACCESSION	AA734458
NID	92801164
KEYWORDS	EST.
SOURCE	Rice.
ORGANISM	<i>Oryza sativa</i>
REFERENCE	Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Eukaryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida; Poales; Poaceae; <i>Oryza</i> .
AUTHORS	1 (bases 1 to 247) Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL	Unpublished (1998)

Contact: Eun M. Y.  
Department of Cytogenetics  
National Inst. Of Agri. Sci. and Tech, RDA  
Suwon, Kyunggido, Korea  
Tel: 82 331 290 0301  
Fax: 82 331 290 0307  
Email: myeun@sun20.asti.re.kr  
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji  
University, Yongin, Korea. 449-728 bhnahe@bioserver.myongji.ac.kr  
Seq primer: M13 Reverse Primer.

```

FEATURES
source
    loc_plane=1;
    loc_reagent=1;
    loc_reagent_frame=1;
    Location/Qualifiers
        1..247
            /organism="Oryza sativa"
            /cultivar="Milyang23"
            /note="Vector: pBluescript SK(+); Site1: EcoRI; Site2:
            XhoI; Directional cDNA library inserted into lambda ZAPIII
            vector at 5' end with EcoRI and 3' end with Xho I site."
            /db_xref="taxon:4530"
            /clone="97SN1784"
            /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
            /tissue tvtype="Immature Seed"

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/dev_stage="5 days after pollination"
/lab_host="E. coli SOUR"
7 a 16 c 21 g 34 t 169 others
BASE COUNT
ORIGIN

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Query Match	0.98;	Score 59;	DB 13;	Length 247;
Best Local Similarity	16.1%;	Pred. No. 6.62e-62;		
Matches	40;	Conservative 119;	Mismatches 83;	Indels 6; Gaps 6;

  

Db	1	HWDCITMNTVVRGCCCCBAWANKKTHMMTBWCCVRRVYGTITNNKGKINGRTTTWDCSDNA	60
Qy	2605	TTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTACTATTCCA-GG-A	2662
Db	61	HCRTVBYIYARSKYGYGTBYISWNVDTNTGGVGKTTVNVHSGWNNRCSNSVYVYVET	120
Qy	2663	GGCGTGGAAACTCTT-CGACTTTCATTCGTGGCCCTATCGCTATTGGAACTGGGACTCG	2721
Db	121	AYCDYBHYBDRANHVDTRCTNDRGVCNTVTSADNGTTSATKRVTVGYDK-TDSDCGGGCGWRK	179
Qy	2722	AGGCTGTCAGAGGTCGTCCGTATTGCGTTCCTTCGATTCGTGCGTGATTCAAACTGG	2781
Db	180	VTYGSSBYRCGVNVVRYRTTSMWTDKSTKMBS-MDMRR-SRVHYGRWMBNKRGRMSRW	237
Qy	2782	CAAAGTCTTGCCCCACACTTAATTACTCATTCATTCGATTATGGGACCCACCATGGGGCGCT	2841
Db	238	TDTKTWET	245
Qy	2842	TGGGTAAT	2849

RESULT	11
LOCUS	AA754458      247 bp      mRNA      EST      20-JAN-1998
DEFINITION	Oryza sativa cv. IR64 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.

ACCESSION	AA754438	
NID	92801164	
KEYWORDS	EST.	
SOURCE	rice.	
ORGANISM	Oryza sativa	
REFERENCE	Eukaryotae; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.	
AUTHORS	N1 (bases 1 to 247) Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.	
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed	
JOURNAL	Unpublished (1998)	
COMMENT		

Contact: Eun M.Y.  
Department of Cytogenetics  
National Inst. of Agri. Sci. and Tech, RDA  
Suwon, Kyunggido, Korea  
Tel: 82 331 290 0301  
Fax: 82 331 230 0307  
Email: myeun@sun20.asti.re.kr  
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji  
University, Yongin, Korea. 449-728 bhna@m bioserver.myongji.ac.kr  
Seg primer: M13 Reverse Primer.

## FEATURES

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SOURCE
Location/Qualifiers
1. .247
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT
7 a 16 c 21 q 34 t 169 others .

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## ORIGIN

Query Match	0.98;	Score 60;	DB 13;	Length 247;
Best Local Similarity	15.88;	Pred. No. 7,47e-64;		
Matches 34;	Conservative 102;	Mismatches 76;	Indels 3;	Gaps 3;
D <b>b</b>	5	TMTNTVWGGCCCBAMNKH-TMMTBBWCVRVGTTNNKGHNGRTTTTNDCSNAHC	R 63	
C <p></p>	3657	TCITATGCGCTACCATATAGAGTTAATGCTGCCAGTGCTGCCTGTAGGACAACTC	3598	
D <b>b</b>	64	Y-TVBYTYARKSYGYGBHYKSWNVDTNTGGTGVGKTVTVNHSGWNRCNSVVYYWBTAI	122	
C <p></p>	3597	TATGGTTTAGCTCGTGTCAGACTATTGTCTTGGTGGGTAAATGTAGTTGCCA-ATCATC	3539	
D <b>b</b>	123	CDVBHYBDRANHHDDTRCTINDRGVCNYTASDNGTSATKRVTGDKTDSDCGGCGWKVKYI	182	
C <p></p>	3538	GTTGCGGTATTAGATAATTGGATTCTTCGGCTTGTGTCTTCATGTCGGCGGTATC	3479	
D <b>b</b>	183	GSSYBYBCGVNVVVRTSMWTDKSTKMBSMDMSRR	217	
C <p></p>	3478	GTGAATTCATTCGATCCCCGATGGCCCACTCCAG	3444	

RESULT	12
LOCUS	AA885211 435 bp mRNA EST 27-MAR-1998
DEFINITION	am34c11.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1468724 3' similar to TR:P70276 SODIUM CHANNEL, TYPE X, ALPHA POLYPEPTIDE ; , mRNA sequence.
ACCESSION	AA885211
NID	q2994288
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 435)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
seq primer: -40md3 fwd. ET from Amersham  
High quality sequence stop: 390.

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FEATURES
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  1. .435
  Location/Qualifiers
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    /note="Organ: pooled; Vector: pT7T3D-pac (Pharmacia) with
    a modified polylinker; Site.1: Not I; Site.2: Eco RI;
    Equal amounts of plasmid DNA from three normalized
    libraries (fetal lung NBLH19W, testis NHT, and B-cell
    NGL-GAP-GBL) were mixed, and ss circles were made in
    vitro. Following HAP purification, this DNA was used as
    tracer in a subtractive hybridization reaction. The driver
    was PCR-amplified cDNAs from pools of 5,000 clones made
    from the same 3 libraries. The pools consisted of
    I.M.A.G.E. clones 297480-302087, 682632-687239,
    726408-728711, and 729096-731399. Subtraction by Bento
    Soares and M. Fatima Bonaldo."
    /db_xref="taxon:9606"
    /clone="IMAGE:1468724"
    /clone_lib="Soares NFL T GBC S1"
    /lab_host="DH10B"
    132 a      89 c      78 g      136 t
BASE COUNT
ORIGIN

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Query Match 0.8%; Score 49; DB 16; Length 435;  
Best Local Similarity 59.5%; Pred. No. 5.67e-43;

Matches	153;	Conservative	0;	Mismatches	104;	Indels	0;	Gaps	0;
Db	16	CAAGGTCGCTGTTTCGACATAGTACAAAGCCAGAGATCTTTGACATCATCATCAATCAAGTCTC	75						
Qy	4893	CAAGCAATAGTCTTTGAAATAGTAAACCGGATAAGAAATTCGATATAATCATTTATGTTATTC	4952						
Db	76	ATTATCTTAACATGATTACGATGATGGCTGAATCATACAAACCAACCCAAAGCCATGAAA	135						
Qy	4953	ATTGGCTGAACATGTTTCACCATGACCCCTCGATCGTTTACGATGGCTGGACAGCTTAAC	5012						
Db	136	TCCATCTCTTGACCATCTCAACTGGGCTCTTTTGCGTCATCTTTACGTAGAAATGCTTCATC	195						
Qy	5013	CGGCTCTTAGACTATCTCAATCGGATATTCGTAGTATTTTTCAGTTCGGAATGCTATTAA	5072						
Db	196	AAATCTTTGCTTTGAGGCATACTACTTCCACCAATGGCTGGAAATTTATTGACTGTGTG	255						
Qy	5073	AAAAATTCGTTTACGATATCACTATTTTATGAGCCATGGAATTTATTGTGATGATGA	5132						
Db	256	GTGCTGCTCTTTTCCAT	272						
Qy	5133	GTTGTCATTTTATCCAT	5149						

RESULT	13
LOCUS	FR0002729      437 bp      DNA      GSS      27-FEB-1997
DEFINITION	F.rubripes GSS sequence, clone 010M03ac8, genomic survey sequence.
ACCESSION	Z66512
NID	G1883424
KEYWORDS	GSS; genome survey sequence.
SOURCE	Fugu rubripes.
ORGANISM	Fugu rubripes Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
REFERENCE	1 (bases 1 to 437)
AUTHORS	Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y., Williams,G. and Brenner,S.
TITLE	Direct Submission
JOURNAL	Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgm.mrc.ac.uk
COMMENT	Vector: ml3mp18 V_type: phage PRIMER: M13 DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

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sequence. Location/Qualifiers
      1. .437
         /organism="Fugu rubripes"
         /db_xref="taxon:31033"
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         /clone="010M03ac8"
BASE COUNT      80 a   159 c   61 g   122 t   5 others
ORIGIN

Query Match      0.8%; Score 50; DB 25; Length 437;
Best Local Similarity 69.6%; Pred. NO. 8.14e-45;
Matches 94; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

Db    301  AGGGATCGTCTCGCCGACATATTGAGAAATACATTTGTGTCGCCGACGTTGTTCCGGGT 360
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy    5153  AGGCTTTGTACTTAGCGATATTATCGAAGTACTTCGTGTGCGCGACCCCTGCTCCGAGT 5212
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db    361  GATTCGATTGGCCGGATCGGAGTATCCTTCGCTCATFCANGGCTGNC AAGGGGTAT -CG 419
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy    5213  GTGCGGTGTGGCGAAAGTGGCCGCTCCTTCGATCGTGTGAAGGAGGCCAAGGGCATTCG 5272
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db    420  GAACCTGCTGTTCCG 434
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy    5273  GACACTGCTCTTCG 5287
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

```

RESULT 14
LOCUS      AA214661      225 bp      mRNA      EST      12-MAR-1998
DEFINITION zq98e09.r1 Stratagene hnt neuron (#937233) Homo sapiens cDNA clone
649192 5' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II
ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION  AA214661
NID         91813315
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 225)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
washed-NCI human EST Project
Unpublished (1997)

Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1023 Std Error: 0.00
Seq Primer: -28m13 rev1 Et from Amersham
High quality sequence stop: 125.
Location/Qualifiers
1..225
/organism="Homo sapiens"
/note="Vector: pbluescript SK-; Site_1: ECORI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hnt neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"
/db_xref="GDB:5278471"
/db_xref="taxon:9606"
/clone="649192"
/clone_lib="Stratagene hnt neuron (#937233)"
/dev_stage="hnt neurons"
/lab_host="SOLR (kanamycin resistant)"
BASE COUNT 54 a 39 c 59 g 72 t 1 others
ORIGIN

Query Match      0.7%; Score 43; DB 16; Length 225;
Best Local Similarity 63.9%; Pred. No. 3.33e-32;
Matches 122; Conservative 0; Mismatches 67; Indels 2; Gaps 2;

Db 28 GTTGGGATTTCTTTTGTGTCAGTTACATCATCATCTTCCTCGTGTGGTGAACATG 87
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5571 GTTGGGAATAAGCTTTCTCCTCTCATACCTAGTTATTAAGCTTTTTCATAGTTATTAATG 5630
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 TACATCGGGTCCTCGGAGCACTTCAGTTGCTACTGAGAAGATGCAGAACCTCTG 147
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5631 TACATTGCTGTCATCTCGGAACATATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTA 5690
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 AGTGAGGATGACTTTGAGCATGTTCCATCAGGTTTGGGAAGAAGTTTGATCCGAATCGGA 207
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5691 ACCGACGACGACTACGACATCTACTATGATCTGGCAGCAA-ITCGATCGGAGGCC-A 5748
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 CCCAGTTTATA 218
||||| |||
QY 5749 CCCAGTACATA 5759

RESULT 15
LOCUS      FR0002750      386 bp      DNA      GSS      27-FEB-1997
DEFINITION F.rubripes GSS sequence, clone 010M03aF9, genomic survey sequence.

```

\*\*\*\*\*  
W P S R L H  
\*\*\*\*\* (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPsrch\_un n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Jul 8 01:39:06 1998; Maspar time 342.93 Seconds  
Tabular output not generated. 1018.955 Million cell updates/sec

Title: >US-08-554-424-7  
Description: (1-6513) from US08554424.seq  
Perfect Score: 6513  
N.A. Sequence: 1 TCTAGACGTTGGCGCATAG.....ACGGAGTATTAGCTCTAGA 6513  
Comp: AGATCTGCAACCGCGTATC.....TGGCTCATAATGAGATCT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0  
Searched: 104157 seqs, 26825796 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-issued  
1:5\_COMB 2: PCT9\_COMB 3: backfiles

Statistics: Mean 10.170; Variance 5.407; scale 1.881

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	2	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
2	6513	100.0	6513	1	US-08-337- Sequence 7, Applicatio	0.00e+00
3	6513	100.0	6513	1	US-08-724- Sequence 7, Applicatio	0.00e+00
4	6513	100.0	6513	1	US-08-338- Sequence 7, Applicatio	0.00e+00
5	6513	100.0	6513	2	PCT-US95-1 Sequence 7, Applicatio	0.00e+00
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7	60	0.9	7218	1	US-08-232- Sequence 14, Applicati	4.19e-23
8	41	0.6	215	1	US-08-238- Sequence 5, Applicatio	1.53e-10
9	36	0.6	215	1	US-08-238- Sequence 5, Applicatio	1.83e-07
10	36	0.6	1809	2	PCT-US95-1 Sequence 1, Applicatio	1.83e-07
11	39	0.6	5904	3	US-07-745- Sequence 6, Applicatio	2.69e-09
12	37	0.6	5962	3	5386025-5 Patent No. 5386025	4.54e-08
13	37	0.6	5975	1	US-08-336- Sequence 3, Applicatio	4.54e-08
14	37	0.6	5975	1	US-08-435- Sequence 1, Applicatio	4.54e-08
15	37	0.6	5975	1	US-08-404- Sequence 1, Applicatio	4.54e-08
16	37	0.6	5975	1	US-08-314- Sequence 1, Applicatio	4.54e-08
17	30	0.5	33	2	PCT-US95-1 Sequence 1, Applicatio	5.74e-04
18	30	0.5	33	2	PCT-US95-1 Sequence 1, Applicatio	5.74e-04
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20	30	0.5	33	1	US-08-337- Sequence 1, Applicatio	5.74e-04

21	30	0.5	33	1	US-08-338- Sequence 1, Applicatio	5.74e-04
22	31	0.5	75	1	Sequence 6, Applicatio	1.56e-04
23	30	0.5	228	3	5482709-9 Patent No. 5482709.	5.74e-04
24	30	0.5	228	3	5273901-10 Patent No. 5273901.	5.74e-04
c	25	0.5	1213	1	US-08-276- Sequence 6, Applicatio	5.74e-04
c	26	0.5	2256	1	US-07-794- Sequence 1, Applicatio	4.18e-05
c	27	0.5	2256	1	US-08-001- Sequence 1, Applicatio	4.18e-05
c	28	0.5	2721	3	5215881-2 Patent No. 5215881.	1.56e-04
29	32	0.5	4255	2	PCT-US96-0 Sequence 14, Applicati	4.18e-05
30	32	0.5	4835	2	PCT-US96-0 Sequence 9, Applicatio	4.18e-05
31	30	0.5	5775	1	US-08-306- Sequence 15, Applicati	5.74e-04
32	30	0.5	5775	2	PCT-US93-0 Sequence 29, Applicati	5.74e-04
c	33	0.5	8438	1	US-07-945- Sequence 1, Applicatio	1.56e-04
c	34	0.4	32	1	US-08-337- Sequence 6, Applicatio	2.07e-03
35	29	0.4	105	1	US-07-865- Sequence 13, Applicati	2.07e-03
36	29	0.4	168	1	US-08-469- Sequence 4, Applicatio	2.07e-03
37	29	0.4	171	1	US-08-469- Sequence 5, Applicatio	2.07e-03
38	29	0.4	1144	1	US-08-486- Sequence 2, Applicatio	2.07e-03
39	29	0.4	1425	1	US-08-385- Sequence 1, Applicatio	2.07e-03
c	40	0.4	2329	2	PCT-US94-0 Sequence 9, Applicatio	2.07e-03
41	29	0.4	3086	3	5206152-1 Patent No. 5206152.	2.07e-03
42	29	0.4	3366	1	US-08-469- Sequence 1, Applicatio	2.07e-03
43	29	0.4	7125	1	US-07-745- Sequence 1, Applicatio	2.07e-03
44	29	0.4	10365	1	US-08-246- Sequence 5, Applicatio	2.07e-03
45	29	0.4	10366	1	US-08-453- Sequence 5, Applicatio	2.07e-03

ALIGNMENTS

RESULT 1  
ID PCT-US95-14378-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx

Sequence 7, Application PC/TUS9514378  
Sequence 7, Application PC/TUS9514378  
GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

APPLICANT: Hall, Linda

APPLICANT: Feng, Gouping

APPLICANT: Van Der Ploeg, Leonardus

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

TITLE OF INVENTION: PARA SODIUM CHANNEL

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Roy D. Meredith

STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14378

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Meredith, Roy D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: 19332 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4678

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6513 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SQ	SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.	
	Query Match 100.0%; Score 6513; DB 2; Length 6513;	
	Best Local Similarity 100.0%; Pred. No. 0.00e+00;	
	Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 TCTAGACGTTGGCGCATAGACATGACAGAAAGATTCGGACTCGATATCTGAGGAAGAAC 60	1021 ACGAGGCACTCTCATTTCCGTTATCGGCAATATATCCGGTCCGGGGCAATGCGACGACG 1080
Qy	1 TCTAGACGTTGGCGCATAGACATGACAGAAAGATTCGGACTCGATATCTGAGGAAGAAC 60	1021 ACGAGGCACTCTCATTTCCGTTATCGGCAATATATCCGGTCCGGGGCAATGCGACGACG 1080
Db	61 GCAGTTTGTTCGTCCTCCCTTACCCTCGAATCATTTGGTGCATAATCGAACAAGCAATCCG 120	1081 ATTACGTTGTCCTGACAGGGTTTGGTCCGAATCCGAATATGGCTACACCAAGCTTCGATT 1140
Qy	61 GCAGTTTGTTCGTCCTCCCTTACCCTCGAATCATTTGGTGCATAATCGAACAAGCAATCCG 120	1081 ATTACGTTGTCCTGACAGGGTTTGGTCCGAATCCGAATATGGCTACACCAAGCTTCGATT 1140
Db	121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCGAGGGAGAGGTGCGCGAT 180	1141 CGTTCCGATGGGCTTTCCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200
Qy	121 CTGAACATGAAAGCAGAGAGCTGGAAAGAAAGAGAGCGAGGGAGAGGTGCGCGAT 180	1141 CGTTCCGATGGGCTTTCCTGTCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200
Db	181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGAGGAGGACGAGGATGAAGTGC 240	1201 TGTACACAGCTGTGTTGTCGCCGCCGCGGACCAATGGCAATGCTGTTCTTATAGTCATCA 1260
Qy	181 ATGGTCGCAAGAAAACAAAAGAAATCCGATATGATGAGGAGGACGAGGATGAAGTGC 240	1201 TGTACACAGCTGTGTTGTCGCCGCCGCGGACCAATGGCAATGCTGTTCTTATAGTCATCA 1260
Db	241 CACACCGGATCCTACACTTGAACAGGCTGTGCCAATACCTGTTGATGTCAGGCGACGT 300	1261 TCTTCTAGTTTCATTTCTATCTGTAATTTGATTTGSCCATTTGTCATGTCGTATG 1320
Qy	241 CACACCGGATCCTACACTTGAACAGGCTGTGCCAATACCTGTTGATGTCAGGCGACGT 300	1261 TCTTCTAGTTTCATTTCTATCTGTAATTTGATTTGSCCATTTGTCATGTCGTATG 1320
Db	301 TCCGCGCGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360	1321 ACGAATTGCAAGAGAGCGCGCAAGAGAGGCTGCCGAAGAGGAGCGATACGTTGAAG 1380
Qy	301 TCCGCGCGAATTTGGCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360	1321 ACGAATTGCAAGAGAGCGCGCAAGAGAGGCTGCCGAAGAGGAGCGATACGTTGAAG 1380
Db	361 TGACATTCGTAGTTGAACCAAGGAAAGATATTTTGGCTTTTCTGCATCAAAAGCAA 420	1381 CGGAAGAAGCTGCCGCCGCCAAAGCTGGAGAGCGGGCCAAATGGCAGGCTC 1440
Qy	361 TGACATTCGTAGTTGAACCAAGGAAAGATATTTTGGCTTTTCTGCATCAAAAGCAA 420	1381 CGGAAGAAGCTGCCGCCGCCAAAGCTGGAGAGCGGGCCAAATGGCAGGCTC 1440
Db	421 TGTGGATGTCGATCCATTCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480	1441 AGCAGCAGCGGATGGGCTGCCGCCGAAGAGGCTGCATCGATCCGGAATGGCCAAAG 1500
Qy	421 TGTGGATGTCGATCCATTCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480	1441 AGCAGCAGCGGATGGGCTGCCGCCGAAGAGGCTGCATCGATCCGGAATGGCCAAAG 1500
Db	481 CATATTTTCCCTATTCATCATCACCAATCTCGTCAACTGCATCTGATGATTAATGC 540	1501 GTCCGAGCTATTCTTGCAATCAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAACGATG 1560
Qy	481 CATATTTTCCCTATTCATCATCACCAATCTCGTCAACTGCATCTGATGATTAATGC 540	1501 GTCCGAGCTATTCTTGCAATCAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAACGATG 1560
Db	541 CGACAAGCCGCGGTTGAGTGCACCTGAGTGTATATTCACCGGAATCTACATTTGAAT 600	1561 ACAACAACAAGAGAAGATGTCATTCGGAGCGCTCGAGGTGGAGTGGAGTCCGTTGAGCG 1620
Qy	541 CGACAAGCCGCGGTTGAGTGCACCTGAGTGTATATTCACCGGAATCTACATTTGAAT 600	1561 ACAACAACAAGAGAAGATGTCATTCGGAGCGCTCGAGGTGGAGTGGAGTCCGTTGAGCG 1620
Db	601 CAGCTGTTAAAGTGATGGCAGAGGTTTCATTTATGCGCGTTACGTTATCTAGAGATG 660	1621 TTATACAAAGAACACCAAGCACTACCAACAGCAGCAGCAACCAAGCTACCAAAAGTTGCTAAAGTGA 1680
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Db	661 CATGGAATTTGGCTGGACTTCGTAGTATAGCTTTAGCTTATGACCATGGGTATAGATT 720	1681 GCACGACATCCTTATCCTTACCTGGTTTACCGTTTACATACGACGAGGATCAGGTAGTT 1740
Qy	661 CATGGAATTTGGCTGGACTTCGTAGTATAGCTTTAGCTTATGACCATGGGTATAGATT 720	1681 GCACGACATCCTTATCCTTACCTGGTTTACCGTTTACATACGACGAGGATCAGGTAGTT 1740
Db	721 TAGTAAATCTAGACGCTCGGAACGTTTAGGTGCTGCGAGCGCTTAAACCGTAGCCA 780	1741 CTCACAAGTACACGATACGGAAACGGAGCTGGCGCTTTGGTATACCCGGTAGCGATCGTA 1800
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Db	781 TTGTGCCAGGCTTCAAGACCATCTGCGCGCGCTGATCGGAATCGGTGAAGAATCTGGCG 840	1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCAGCTTCCCTATGCCCAGCACT 1860
Qy	781 TTGTGCCAGGCTTCAAGACCATCTGCGCGCGCTGATCGGAATCGGTGAAGAATCTGGCG 840	1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCAGCTTCCCTATGCCCAGCACT 1860
Db	841 ATGTGATTATCCTGACCATGTTCTCCCTGTCGGTGTTCGGTGTGATGGGCTACAGATCT 900	1861 CGAATGCCGTCACCCGATGTCGGAAGAGATGGGCCATCATAGTGCCTGTACTATG 1920
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Db	901 ATATGGGCGTCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGGAGCGTTCTTGGGCA 960	1921 GCAATCTAGGCTCCCGACACTCATGATACCTGCATCAGTCCGGAATATCGTATACCT 1980
Qy	901 ATATGGGCGTCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGGAGCGTTCTTGGGCA 960	1921 GCAATCTAGGCTCCCGACACTCATGATACCTGCATCAGTCCGGAATATCGTATACCT 1980
Db	961 ATCTGACCGAGAGACTGGGACTATCACATCGCAATAGCTCCAAATGGTATTCCGAGG 1020	1981 CACATGGGATCTACTCGCGGCTGTCATGGGCTCAGCACAAATGACCAAGGAGA 2040
Qy	961 ATCTGACCGAGAGACTGGGACTATCACATCGCAATAGCTCCAAATGGTATTCCGAGG 1020	1981 CACATGGGATCTACTCGCGGCTGTCATGGGCTCAGCACAAATGACCAAGGAGA 2040

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Qy 2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAAATCCCTTTATCGAGCCCGTCCAGACAC 2220  
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Qy 2221 AAACGGTGGTGTGATPATAAAGATGTGATGTCCTGTAATGACATCATCGAACAGGCCGCTG 2280  
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Qy 2641 GCCCAAGTACTATTTCCAGAGGGCTGGACATCTTCGACTTCATTTATCGTGGCCCTAT 2700  
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Qy 2701 CGCTATTGGAACCTGGGACTCGAGGGTGTCCAGGGTGTCTCGGTATTCGGTTCCTTCGAT 2760  
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Qy 2881 TCTTTGGGGTGATGGGAATGCAACTGTTGGAAAGAAATATCATGATCACAAGGACCGCT 2940  
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Qy 2941 TTCGGATGGCGACCTGCCGCGCTTGGAACTTCACCGACTTTATGCACAGCTTCATGATCG 3000  
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Qy 3001 TGTTCGGGTGCTCTGGGGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG 3060  
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Qy 3421 AGGGGATCAAGGAGCAGACCAACTGGAGGTGCCATCGGGGATCGGATGGAATTCACGA 3480  
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Qy 4141 GCTTCAAGTGTACTTCCACCAACGCGTGTGTTGGCTCGATTTTCGATTTGTCATGTAT 4200  
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QY 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG 4620  
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QY 4621 CTATCGATTTCAGAGAGTGGACAGCAACCAATTCGTTGAACGAACATCTACATGTATT 4680  
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Db 6481 CCCTCAAGATGACGCGAGTATTAGCTCTAGA 6513  
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6481 CCCTCAAGATGACGCGAGTATTAGCTCTAGA 6513  
RESULT 2  
ID US-08-337-339-7 STANDARD; DNA; UNC; 6513 BP.  
AC XXXXX  
DE Sequence 7, Application US/08337339  
CC Sequence 7, Application US/08337339  
CC Patent No. 5593864  
CC GENERAL INFORMATION:  
CC APPLICANT: Warnke, Jeffrey W.  
CC APPLICANT: Hall, Linda  
CC APPLICANT: Feng, Gouping  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: John W. Wallen III  
CC STREET: P. O. Box 2000, 126 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0900  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/337,339  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Wallen III, John W.  
CC REGISTRATION NUMBER: 35,403  
CC REFERENCE/DOCKET NUMBER: 19332  
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CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.  
Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 TCTAGAGCTTGGCGCGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAAGAAC 60  
QY |||||||||||||||||||||||||||||||||||||||  
1 TCTAGAGCTTGGCGCGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAAGAAC 60  
Db 61 GCAGTTGTTCCGTCCTTTACCCGCGGAATCATTTGGTGCAATCGAACACAGCATTCGCG 120  
QY |||||||||||||||||||||||||||||||||||||||  
61 GCAGTTGTTCCGTCCTTTACCCGCGGAATCATTTGGTGCAATCGAACACAGCATTCGCG 120  
Db 121 CTGAACATGAAGACAGAGAGCTGGAAGAAAGAGAGCGGAGAGAGGTGCGCGAT 180  
QY |||||||||||||||||||||||||||||||||||||||  
121 CTGAACATGAAGACAGAGAGCTGGAAGAAAGAGAGCGGAGAGAGGTGCGCGAT 180  
Db 181 ATGTCGCAAGAAAAACAAAAAATCCGATATGATGACGAGGACGAGATGAAGGTC 240  
QY |||||||||||||||||||||||||||||||||||||||  
181 ATGTCGCAAGAAAAACAAAAAATCCGATATGATGACGAGGACGAGATGAAGGTC 240  
Db 241 CACAAACGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTCCGATTCGAGGGCAGCT 300

QY 241 CACAAACGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTGCGAGGGCAGCT 300  
Db 301 TCCCGCGGAATGGCCTCCACTCCCTCTCAGGATATCGATCCCTACTACAGCAATGTAC 360  
QY |||||||||||||||||||||||||||||||||||||||  
301 TCCCGCGGAATGGCCTCCACTCCCTCTCAGGATATCGATCCCTACTACAGCAATGTAC 360  
Db 361 TGACATTCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTCTGTCATCAAAAGCAA 420  
QY |||||||||||||||||||||||||||||||||||||||  
361 TGACATTCGTAGTTGTAAGCAAGAAAGATATTTTCGCTTTCTGTCATCAAAAGCAA 420  
Db 421 TGTGGATGCTCGATCCATTCATCCGATACGTCGTGCGCATTTACATTTAGTGCATC 480  
QY |||||||||||||||||||||||||||||||||||||||  
421 TGTGGATGCTCGATCCATTCATCCGATACGTCGTGCGCATTTACATTTAGTGCATC 480  
Db 481 CATTAATTTCCCTATTTCATCATCACCACAAATTCCTCGTCAACTGCATCCCTGATGATATGC 540  
QY |||||||||||||||||||||||||||||||||||||||  
481 CATTAATTTCCCTATTTCATCATCACCACAAATTCCTCGTCAACTGCATCCCTGATGATATGC 540  
Db 541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACATTTGAAT 600  
QY |||||||||||||||||||||||||||||||||||||||  
541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACATTTGAAT 600  
Db 601 CAGCTGTTAAAGTGATGGCAGAGGTTTCATTTATGCGCGTTTACGTATCTTAGAGATG 660  
QY |||||||||||||||||||||||||||||||||||||||  
601 CAGCTGTTAAAGTGATGGCAGAGGTTTCATTTATGCGCGTTTACGTATCTTAGAGATG 660  
Db 661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTATGACCATGGGTATAGAT 720  
QY |||||||||||||||||||||||||||||||||||||||  
661 CATGGAATGGCTGGACTTCGTAGTAATAGCTTATGACCATGGGTATAGAT 720  
Db 721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGTTGTCGAGCGCTTAAACCGTAGCCA 780  
QY |||||||||||||||||||||||||||||||||||||||  
721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGTTGTCGAGCGCTTAAACCGTAGCCA 780  
Db 781 TTGTGCAGGCTTGAAGACCATCGTCGCGCGCTCATCGAATCGGTGAGAAATCTCGCG 840  
QY |||||||||||||||||||||||||||||||||||||||  
781 TTGTGCAGGCTTGAAGACCATCGTCGCGCGCTCATCGAATCGGTGAGAAATCTCGCG 840  
Db 841 ATGTGATTATCTTGACCATGTTCTCCCTGTCGCTGTTCCGCTTGATGGGCTACAGATCT 900  
QY |||||||||||||||||||||||||||||||||||||||  
841 ATGTGATTATCTTGACCATGTTCTCCCTGTCGCTGTTCCGCTTGATGGGCTACAGATCT 900  
Db 901 ATATGGCGTGTCCACGAGAGTGCATCAAGAAAGTTCCGCTGGAGCGTTCTCGGGGCA 960  
QY |||||||||||||||||||||||||||||||||||||||  
901 ATATGGCGTGTCCACGAGAGTGCATCAAGAAAGTTCCGCTGGAGCGTTCTCGGGGCA 960  
Db 961 ATCTGACCGACGAGAACTGGGACTATCACATCGCAATAGCTCCAATGGTATTCGAGG 1020  
QY |||||||||||||||||||||||||||||||||||||||  
961 ATCTGACCGACGAGAACTGGGACTATCACATCGCAATAGCTCCAATGGTATTCGAGG 1020  
Db 1021 ACGAGGCACTCTCATTTCCGTTATGCGCAATATATCCGGTGGGGGCAATGGAGCAGC 1080  
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1021 ACGAGGCACTCTCATTTCCGTTATGCGCAATATATCCGGTGGGGGCAATGGAGCAGC 1080  
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1081 ATTACGTGTCCCTGACAGGGTTTGGTCCGAATCCGAATATGGCTACACAGCTTCGATT 1140  
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QY 1321 ACGAATTGCAAGGAGCGCCGAAAGAAAGAGAGCTGCCGAAGAGGAGCGCATACGTGAAG 1380  
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QY 1381 CGAAGAGCTGCGCGCCGCAAAAGCGCCAAAGCTGAGGAGCGGCGCAATGCGCAGGCTC 1440  
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QY 1441 AGGCAGAGCGGATGCGGCTGCGCGCCGCAAAAGCGCTGCACTCGGAAATGGCCAAAGA 1500  
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QY 1501 GTCCGAGCTATCTTGATCAGCTATGAGCTATTTGTTGCGCGGAGGAGGCAACGATG 1560  
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QY 1561 ACAACAACAAGAGAAGATGTCATTCGGAGCGTCGAGGTGGAGTGGAGTGGAGTGGAGCG 1620  
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QY 1621 TTATACAAGACAACGACACCTACACAGCACACCAAGCTACCAAGTTTCGTAAGCTGA 1680  
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QY 1681 GCACGACATCTTACCTTACCTGCTTACCGTTTAAACATACGAGGAGGATCAGTATGTT 1740  
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QY 1741 CTCACAAGTACAGATACGGAACGAGCTGGCGGTTTGGTATACCGGTAGCGATCGTA 1800  
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QY 1801 AGCCATGTTGATGTCACATATACGATACGAGTACGAGTACGAGTACGAGTACGAGTACG 1860  
Db 1861 CGAATCCGCTACCGGATGTCGGAAGAGATGGGCGCATCATAGTGGCGGTGACTATG 1920  
QY 1861 CGAATCCGCTACCGGATGTCGGAAGAGATGGGCGCATCATAGTGGCGGTGACTATG 1920  
Db 1921 GCAATCTAGGCTCCGACACTCATGATACCTGATCAGTACGATCAGTACGATCAGTACCT 1980  
QY 1921 GCAATCTAGGCTCCGACACTCATGATACCTGATCAGTACGATCAGTACGATCAGTACCT 1980  
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QY 1981 CACATGCGATCTACCTGCGGATGTCGCGGATGTCGCGGATGTCGCGGATGTCGCGGATG 2040  
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QY 2041 GCAATTTGCGCAACCGCAACACACAGCAATCAATCAGTGGCGCCACCAATGGCGGACCA 2100  
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QY 2101 CCGTCTGCGACCAATCAACAAGCTGATCATCGGACTACGAAATGGGCTGGAGTGA 2160  
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QY 2161 CGGACGAGCTGGCAAGATTAACATCATGACATCCTTTTATCGAGCCGCTCCAGACAC 2220  
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QY 2221 AAACGGTGGTGTATGAAGATGTGATGCTGCTGATGATCATCATGCAACAGCGCGCTG 2280  
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QY 2281 GTCCGACAGTCGCGGACGAGCTACGCGGTGCTCGGTTTACTATTTCCCAACAGAGAGC 2340  
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QY 2341 ATGACGAGATGGCGGACGCTTCAAGACAAGGACATCGAGTATCTCAAAAGGATCG 2400  
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QY 2401 ATGCTGTTTGTGTGGGACTGTTGCTGGGTTTGGTGTGAAATTTTCAAGAGTGGGTATCGC 2460

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QY 2461 TCATCGTCTTCGATCCCTTCGAGCTCTTCATCAGCTGTGCATTTGGTGTGCTCAACACGA 2520  
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QY 2521 TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGGAACGCGTCTCAAGAGTG 2580  
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QY 2581 GCAACTATTTCTCACCGCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
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QY 2641 GCCCAAGTACTATTTCCAGGAGGCTGGACATCTTCGACTTCATTTATCGTGCCCTAT 2700  
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QY 2761 TGCTGCTGTTTCAAACTGGCCAAAGTCTTGCCCCACACTTTAAATTTACTCAATTCGATTA 2820  
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QY 2821 TGGAGCGCACCATGGGCGCTTTGGGTAACTGACATTTGTACTTTGCAATTTATCATCTTCA 2880  
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QY 2881 TCTTTCCGCTGATGGAAATGCAACTGTTGCGGAAGAATTTATCATGATCACAAGGACCGCT 2940  
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QY 3061 ATGCTCTGCTCATTCCTTCTTGGCCACCGTTCATCGGCAATCTTGTGGTACTTA 3120  
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QY 3181 CCGATAACGATACGAATAAATAGCCGAGGCTTCATCGAATTTGGCCGATTTAAAGTT 3240  
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QY 3301 TAAGTATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTGGAGGGAAGAGC 3360  
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QY 3361 ATGTTGACAACGAACTGGAGCTGGCCACGAGAGATCTCGCGGAGGCTCATCAAGA 3420  
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QY 3421 AGGGATCAAGAGGACGCAACTGGAGGTGGCCATCGGGATCGGATGGAATTCACGA 3480  
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QY 3481 TACACGGGACATGAAGAACCAACAGCGGAAAGAAATCCAAATATCTAAATACCGCAACGA 3540

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Db 5101 TTATTCAGCCATCGAATTTATTTGATGTAGTGTCTATTTTATCCATCTTAGTCTTTG 5160  
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Db 5341 TCATGTTTCATCTTTGCCATTTTCGGCATGCTGTTTTCATGACGTTGAAGGAGAGCG 5400  
QY |||||||TCATGTTTCATCTTTGCCATTTTCGGCATGCTGTTTTCATGACGTTGAAGGAGAGCG 5400  
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QY 5941 AGGAGACGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
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QY 6001 TCTCATCAACCTGTGCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 6060  
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QY 6301 CGCGCGCGCGGACGACGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 6360  
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QY 6361 CGCGCGCTTCTGCTGAGAGCGAGCGGTTGCTGACGAGAACGCGGCGGACGAGTGTGAGTGTGAGT 6420  
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Db 6481 CCTCCAGATGACGCGAGTATTAGTCTTAGA 6513  
QY 6481 CCTCCAGATGACGCGAGTATTAGTCTTAGA 6513

RESULT 3  
ID US-08-724-095-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx  
DE  
Sequence 7, Application US/08724095  
CC Sequence 7, Application US/08724095  
CC Patent No. 5688917  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Hall, Linda  
CC APPLICANT: Feng, Gouping  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: J. Mark Hand - Merck & Co., Inc.  
CC STREET: P.O. Box 2000 - 126 E. Lincoln Avenue

CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0907  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTseq. Version #1.d5  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/724,095  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Hand, J. Mark  
CC REGISTRATION NUMBER: 36,545  
CC REFERENCE/DOCKET NUMBER: 19332DA  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-3905  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 1 TCTAGAGCTGGCGCGATAGACAAATGACAGAAGATCCGACCTCGATATCTAGAGGAAGAC 60  
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Db 181 ATGGTCCGAGAAAACAAAAGAAATCCGATATCATGACGAGGACGAGGATGAAGTGC 240  
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Qy 1561 ACAACAAGAGAGAGATGTCATTCGAGCGTCGAGGTGGAGTCCGAGTCCGAGTACG 1620  
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Qy 1621 TTATACAAAGACCAACGACCTACCAAGCAGCACACCAAGCTTACCAAGTTTCGTAAGTGA 1680  
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Qy 1681 GCACGACATCCTTATCCTTACCTGGTTTACCGTTTAAACATACGAGGGATCACGTAGTT 1740  
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Qy 1801 AGCCATTGGTATTGTTCAACATATCAGATGCCAGAGCACTTGGCCCTATGCGGAGACT 1860  
Db 1861 CGAATCCGTCACCCCGATGTCGGAAGAGAAATGGGCCATCATAGTGGCCGTACTATG 1920  
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Db 1921 GCAATCTAGCTCCCGACACTCATCTATACCTTCGATCAGTCCCGAATATCTATACCT 1980  
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Qy 2101 CCGTCTTGGACACCAATCACAAGCTCGATCATCGGACTACGAAATTTGGCCTGGAGTGA 2160  
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Qy 2521 TGTTCATGGCAATGGATCACACGATATGAACGAGAGATGGAACGCTGCTCAAGAGTG 2580  
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Qy 2581 GCAACTATTTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
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Qy 2641 GCCCAAGTACTATTTCCAGGAGGCTTGGAAACATCTTCGACTTCATTCGTCGTCCTAT 2700  
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Qy 2701 CGCTATTGGAACCTGGGACTCGAGGGTGTCCAGGGTCTGTCGCTATTGCGTTCCTTCGAT 2760  
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Qy	2761	TGTCGCGTGATTCAAACACTGCCCAAGTCTTTGGCCCAACACTAAATTTACTCATTTTCGATTA	2820
Db	2821	TGGACGCACCATGGCGCTTTGGGTAATCTGACATTTGTACTTTTGCATTTATCATCTTCA	2880
Qy	2821	TGGACGCACCATGGCGCTTTGGGTAATCTGACATTTGTACTTTGCAITTTATCATCTTCA	2880
Db	2881	TCITTTGGCGTGATGGGAATGCAACTGTTTCGGAAGAATTAATCATGATCACAGACCGCT	2940
Qy	2881	TCITTTGGCGTGATGGGAATGCAACTGTTTCGGAAGAATTAATCATGATCACAGACCGCT	2940
Db	2941	TTCCGGATGGGCACTGCCGCGTGGAACTTTCACCGACTTTATGSCACAGCTTTCATGATCG	3000
Qy	2941	TTCCGGATGGGCACTGCCGCGCTGGAACTTTCACCGACTTTATGSCACAGCTTTCATGATCG	3000
Db	3001	TGTTCCGGGTCTCTGGCGAGAATGGATCGAGTCCATGTGGGACTGCAATGAGTGGGCG	3060
Qy	3001	TGTTCCGGGTCTCTGGCGAGAATGGATCGAGTCCATGTGGGACTGCAATGAGTGGGCG	3060
Db	3061	ATGTCCTGTGATTCCTTCTTCTTGGCCACCGTTGTCATCGGCAACTTGTGTGTACTTA	3120
Qy	3061	ATGTCCTGTGATTCCTTCTTCTTGGCCACCGTTGTCATCGGCAACTTGTGTGTACTTA	3120
Db	3121	ACCTTTTCTTAGCCTTGCTTTTGTCCAAATTTTGGCTCACTAGTCTATFACGCGCGACTG	3180
Qy	3121	ACCTTTTCTTAGCCTTGCTTTTGTCCAAATTTTGGCTCACTAGTCTATFACGCGCGACTG	3180
Db	3181	CCGATAACGATPAGAAATAAATAGCCGAGGCCCTTCAATCGAATTTGGCGATTTTAAAGTT	3240
Qy	3181	CCGATAACGATPAGAAATAAATAGCCGAGGCCCTTCAATCGAATTTGGCGATTTTAAAGTT	3240
Db	3241	GGTTPAAGCGTAATATTGCTGATTTCTTCAAGTTAATACGTAACAAATTGACAATCAAA	3300
Qy	3241	GGTTPAAGCGTAATATTGCTGATTTCTTCAAGTTAATACGTAACAAATTGACAATCAAA	3300
Db	3301	TAAGTGATCAACCATCAGGTGAGAGCAACCAACAGATCAGTTGGATTTGGAGCGAAGAGC	3360
Qy	3301	TAAGTGATCAACCATCAGGTGAGAGCAACCAACAGATCAGTTGGATTTGGAGCGAAGAGC	3360
Db	3361	ATGGTCACACGAACCTGGAGCTGGGCCAGCAGAGATCCTCGCCAGACGGCCTCATCAAGA	3420
Qy	3361	ATGGTCACACGAACCTGGAGCTGGGCCAGCAGAGATCCTCGCCAGACGGCCTCATCAAGA	3420
Db	3421	AGGGGATCAAGGACGACGCAACTCGAGGTGGCCATCGGGGATCGGATGGAATTCAGA	3480
Qy	3421	AGGGGATCAAGGACGACGCAACTCGAGGTGGCCATCGGGGATCGGATGGAATTCAGA	3480
Db	3481	TACACGGCGACATGAAGAACAACAACGGAAGAAATCCAAATATCTAAATAACGCAACGA	3540
Qy	3481	TACACGGCGACATGAAGAACAACAACGGAAGAAATCCAAATATCTAAATAACGCAACGA	3540
Db	3541	TGATTTGGCAACTCAATTAACCCCAAGACAATAGACTGGAAACACGAGCTTAACCATAGAG	3600
Qy	3541	TGATTTGGCAACTCAATTAACCCCAAGACAATAGACTGGAAACACGAGCTTAACCATAGAG	3600
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Qy	3601	GTTTGTCTTACAGGACGACGACTGCCAGCATTAACATCATGTAGGCCATAAGAAATC	3660
Db	3661	GACCATTAAGGACGAGAGCCACAAGGGCAGCCCGAGAGCATGTGAGGGCGAGGAGAAGC	3720
Qy	3661	GACCATTAAGGACGAGAGCCACAAGGGCAGCCCGAGAGCATGTGAGGGCGAGGAGAAGC	3720
Db	3721	CGGACGCCAGCAGAGGATTTAGGTCTCCACGAGGAACCTGGACGAGGAGGGCGAATGCG	3780
Qy	3721	CGGACGCCAGCAGAGGATTTAGGTCTCCACGAGGAACCTGGACGAGGAGGGCGAATGCG	3780
Db	3781	AGGAGGGCCCGCTCGACGGTGATATCATTAATTCATGACACGACGAGGATATACTCGATG	3840
Qy	3781	AGGAGGGCCCGCTCGACGGTGATATCATTAATTCATGACACGACGAGGATATACTCGATG	3840
Db	3841	AATATCCAGCTGATTTGTCGCCCGCGATTCGTACTATAGAAATTTCCCATCTTAGCCGGTG	3900
Qy	3841	AATATCCAGCTGATTTGTCGCCCGCGATTCGTACTATAGAAATTTCCCATCTTAGCCGGTG	3900

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Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy																																																																																																																																																													
RCGATGACTCGCGTTC	CGGTTCTGGCAAGATGGGCAATTTACGACTGAAACATTTTCAATTAA			RCGATGACTCGCGGTT	CTGGCAAGATGGGCAATTTACGACTGAAACATTTTCAATTAA			TTGAAAATAAATATTT	TGAAACAGCTGTATACATATGATTTTAA	TGAGTAGAGATGTACAT	CTGCCACAAAGACCCATCTCAGGATATTTTATACATATA			TGCGATTAGAAGATGTACAT	CTGCCACAAAGACCCATCTCAGGATATTTTATACATATA			TGGCAGATAATTTT	TCGGTTATATCTTCTTGGAAATGTTAAT	CAAGTGGTTGGCGTCG	4140	4140			GCTTCAAGTGTACTT	TCACCAACGGTGGTGTGGCTCGATTTGCTGATATGCTCATGTAT	4200	4200	GCTTCAAGTGTACTT	TCACCAACGGTGGTGTGGCTCGATTTGCTGATATGCTCATGTAT	4200	4200			CGCTTATCAACTTCG	TGCTTCCACTTGTGGAGCTGGTGGTATTC	CAAGCCTTCAGACTA	4260	4260			CGCTTATCAACTTCG	TGCTTCCACTTGTGGAGCTGGTGGTATTC	CAAGCCTTCAGACTA	4260	4260			TGCGAAGCTTTAGACACAT	TCAGACACATACGTCGCTATGCCGATTCAGGCGCATGAGG	4320	4320			TGCGAAGCTTTAGACACAT	TCAGACACATACGTCGCTATGCCGATTCAGGCGCATGAGG	4320	4320			TCGTCGTTAATCGCT	TGGTACAGCTATACCGTCCATCTCAATGTGCTATTTGGTGTGTC	4380	4380			TCGTCGTTAATCGCT	TGGTACAGCTATACCGTCCATCTCAATGTGCTATTTGGTGTGTC	4380	4380			TATATTTTGGCTAA	TTTTTGGCCATTAATGGGTACAGCTTTTTCGTGAAAAATATTTTA	4440	4440			TATATTTTGGCTAA	TTTTTGGCCATTAATGGGTACAGCTTTTTCGTGAAAAATATTTTA	4440	4440			AGTCGAGGACATGAT	GGCAGCAAGCTCAGCCACAGAGATACACAAATCGCAATGCCT	4500	4500			AGTCGAGGACATGAT	GGCAGCAAGCTCAGCCACAGAGATACACAAATCGCAATGCCT	4500	4500			CGGAGCGGAGAACTAC	ACGTGGGTGAATTCAGCATGAATTCGATCATGTAGGTAAAG	4560	4560			CGGAGCGGAGAACTAC	ACGTGGGTGAATTCAGCATGAATTCGATCATGTAGGTAAAG	4560	4560			CGTATCTGTGCTTT	CTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620	4620			CGTATCTGTGCTTT	CTTCCAAAGTGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG	4620	4620			CTATCGAATTCAGAGAG	GTGACCAAGCAACCAATTCGTGAAACGACATCTACATGTAT	4680	4680			CTATCGAATTCAGAGAG	GTGACCAAGCAACCAATTCGTGAAACGACATCTACATGTAT	4680	4680			TATATTTTGGTAT	TTCTTCATCATATTTTGGATGCTTTTTCACACTCAATCTGTTTCAATGGTG	4740	4740			TATATTTTGGTAT	TTCTTCATCATATTTTGGATGCTTTTTCACACTCAATCTGTTTCAATGGTG	4740	4740			TTATCATTTGATAA	TTTTTAAATGAGCAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTCA	4800	4800			TTATCATTTGATAA	TTTTTAAATGAGCAAAAGAAAAAGCAGGTGGATCATTTAGAAATGTTCA	4800	4800			TCACAGAGATCAGAAA	AGTACTATATGCTATGAAAAGATGGGCTCTAAAAAAACCAT	4860	4860			TCACAGAGATCAGAAA	AGTACTATATGCTATGAAAAGATGGGCTCTAAAAAAACCAT	4860	4860			TAAAAGCCATTCCA	AGACCAAGGTGGCGACCAACAGCAATAGTCTTTGAAATAGTACCG	4920	4920			TAAAAGCCATTCCA	AGACCAAGGTGGCGACCAACAGCAATAGTCTTTGAAATAGTACCG	4920	4920			ATAAGAAATTCATAT	TAATCATTTATGTTATTCATTTGGTCTGAAATGTTTACCATGACCC	4980	4980			ATAAGAAATTCATAT	TAATCATTTATGTTATTCATTTGGTCTGAAATGTTTACCATGACCC	4980	4980			ATAAGAAATTCATAT	TAATCATTTATGTTATTCATTTGGTCTGAAATGTTTACCATGACCC	4980	4980		



Db 4981 TCGATCGTTACGATCGCTCGACAGCTATACAGCGGTCCTAGACTATCTCAATCCGATAT 5040  
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RESULT 4  
ID US-08-338-702-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxx  
DT  
DE Sequence 7, Application US/08338702  
CC Sequence 7, Application US/08338702  
CC Patent No. 5550049  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: John W. Wallen III  
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0900  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/338,702  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Wallen III, John W.  
CC REGISTRATION NUMBER: 35,403  
CC REFERENCE/DOCKET NUMBER: 19338  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-3905  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single

CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA  
SQ SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.  
Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCTAGACGTTGGCCGATAGACAAATGACAGAAAGATTCGGACTCATATCTGAGGAAGAAC 60  
Qy 1 TCTAGACGTTGGCCGATAGACAAATGACAGAAAGATTCGGACTCATATCTGAGGAAGAAC 60  
Db 61 GCAGTTTCTCGTCCCTTTACCCGCGAATCATTTGGTCAAAATCGAAACAGCGATTCCG 120  
Qy 61 GCAGTTTCTCGTCCCTTTACCCGCGAATCATTTGGTCAAAATCGAAACAGCGATTCCG 120  
Db 121 CTGAACATGAAAGCAGAGAGCTGGAAGAAAGAGAGAGCGAGGAGAGTGCCTGGAT 180  
Qy 121 CTGAACATGAAAGCAGAGAGCTGGAAGAAAGAGAGAGCGAGGAGAGTGCCTGGAT 180  
Db 181 ATGGTCGCAAGAAAACAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTTC 240  
Qy 181 ATGGTCGCAAGAAAACAAAGAAATCCGATATGATGACGAGGACGAGATGAAGTTC 240  
Db 241 CACAACCGGATCTTACACTTGAACAGGGTGTGCCAATACCTTTCGATTGCGAGGSCAGCT 300  
Qy 241 CACAACCGGATCTTACACTTGAACAGGGTGTGCCAATACCTTTCGATTGCGAGGSCAGCT 300  
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Qy 301 TCCCGCGGAATGGCCCTCCACTCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360  
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Qy 481 CATTATTTCCCTATTTCATCATCACCAATCTCTGCACTGCATCCCTGATGATTAATGC 540  
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Qy 961 ATCTGACCGCAGGAACTGGGACTATCACAATCGCAATAGCTCCAATTTGGTATTCGAGG 1020  
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RESULT 5

ID PCT-US95-14262-7 STANDARD; DNA; UNC; 6513 BP.

AC xxxxxx

DT Sequence 7, Application PC/TUS9514262

DE Sequence 7, Application PC/TUS9514262

CC GENERAL INFORMATION:

CC APPLICANT: Warmke, Jeffrey W.

CC APPLICANT: Van Der Ploeg, Leonardus

CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

CC TITLE OF INVENTION: PARA SODIUM CHANNEL

CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Jack L. Tribble

CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CC CITY: Rahway

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 07065-0907

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US95/14262

CC FILING DATE:

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Tribble, Jack L.

CC REGISTRATION NUMBER: 32,633

CC REFERENCE/DOCKET NUMBER: 19338 PCT

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CC INFORMATION FOR SEQ ID NO: 7:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 6513 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: CDNA

SQ SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match 100.0%; Score 6513; DB 2; Length 6513;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Q	y	3121	ACCTTTCTTACGCTTGTCTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180
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3901 ACGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTA 3960  
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3961 TTGAAATAAATATTTTGAACAGCTGTTATCACTATGATTTTAAATGAGTAGCTTAGCTT 4020  
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4141 GCTTCAAAGTGTACTTCAACACGCTGTTGGCTCGATTTTCTGATTTGTCATGCTAT 4200  
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4201 CGCTATCAACTTCGTTCTACCTTGTGGAGCTGTGTATTCAGCCCTTCAAGACTA 4260  
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4261 TGGCAAGCTTAAGAGCACTGAGACCACTACGTGCAATGTCCTGATCGAGGCAATGAGG 4320  
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5581 CGTTCTCTCTCATACCTAGTTTATAGCTTTTGTAGTTTATTAATATGATACATGCTG 5640  
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5701 ACTACGACATGTACTATGAGATCTGCGCAATTCGATCCGGAGGGGCCACCATATAC 5760  
5701 ACTACGACATGTACTATGAGATCTGCGCAATTCGATCCGGAGGGGCCACCATATAC 5760





GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFELINGER, F. G.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F1s  
SEQUENCE 7218 BP: 1944 A: 1491 C: 1486 G: 1929 T: 36

RESULT	8	
ID	US-08-238-163-5	STANDARD; DNA; UNC; 215 BP.
AC	xxxxxx	
DT	Sequence 5,	Application US/08238163
DE	Sequence 5,	Application US/08238163
CC	Patent No. 5569830	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	BENNETT, Alan
CC	APPLICANT:	LABAVITCH, John M.
CC	APPLICANT:	POWELL, Ann
CC	APPLICANT:	STOFZ, Henrik
CC	TITLE OF INVENTION:	PLANT INHIBITORS OF FUNGAL
CC	TITLE OF INVENTION:	POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC	NUMBER OF SEQUENCES:	24
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Townsend and Townsend Khourie and Crew
CC	STREET:	Steuart Street Tower, One Market Plaza
CC	CITY:	San Francisco
CC	STATE:	California
CC	COUNTRY:	US
CC	ZIP:	94105-1493
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	US/08/238,163
CC	APPLICATION NUMBER:	US/08/238,163
CC	FILING DATE:	03-MAY-1994
CC	CLASSIFICATION:	800
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Bastian, Kevin L.
CC	REGISTRATION NUMBER:	34,774
CC	REFERENCE/DOCKET NUMBER:	2307E-540
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(415) 543-9600
CC	TELEFAX:	(415) 543-5043
CC	INFORMATION FOR SEQ ID NO:	5:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	215 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	unknown
CC	MOLECULE TYPE:	protein
CC	FEATURE:	
CC	NAME/KEY:	misc_feature
CC	LOCATION:	1..215
CC	OTHER INFORMATION:	/standard_name= "Deduced amino acid
CC	OTHER INFORMATION:	sequence of PGIP from bean."
CC	SEQUENCE	215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
Qy	Query Match	0.6%; Score 41; DB 1; Length 215;
Qy	Best Local Similarity	15.6%; Pred. No. 1.53e-10;
Qy	Matches	30; Conservative 77; Mismatches 83; Indels 2; Gaps 2;
Db	22	AKKGNTSSWTTDCCNRTWGVCDTDTYRVNDSGHNKYSSANYTGGNVGAAKTHYY 81
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Db	82	THTVSGADSKTVVDSYNASGCTSSSNGTDCNRSADSYGSSKTA-WTSRNRRTGKTANNA 140
Qy	1317	TATGACGAATTCGAAGAAGAGCCGCAAGAGAGAGCTGCCGAAGAGGAGGCGATACGT 1376
Db	141	VDSRNMGDASVGSBKNTKKHAKNSADGKSGKNNGDRNNRYGTGKTNSVSNCCGGNKR 200
Qy	1377	GAAGCGGAAGAGCTCGCGCGCCAAAGCGCCCAAGCTGGAG-GAGCGGGCCAATGCGCA 1435
Db	201	VSSYANKKCGS 212
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RESULT 9
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx

DE Sequence 5, Application US/08238163
DE Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOFZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLIGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Stewart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238,163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
CC SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
SQ

Query Match 0.68; Score 36; DB 1; Length 215;
Best Local Similarity 16.9%; Pred. No. 1.83e-07;
Matches 27; Conservative 61; Mismatches 72; Indels 0; Gaps 0;

Db 1 MTNVTSSSVSWRTASCDKAKKDGNTSSWTTDCCNRTWGYCDTDTTYRVNNDSGHNK 60
Cp 233 ATCTCTCTCTCGTCATCATCGGATCTCTTTTCTTTTCTTCTCGGACCATATCGCGG 174
Db 61 YSSANYGNNGNVAATHYTHTVNSGADSKVTVTSYNASGTSSSNGTGNRSGADSY 120
Cp 173 CACCTCTCCCTCGGCTCTCTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 114
Db 121 GSSKTATSRNRGKTANNVDSNRNMGDASVGDKNK 160
Cp 113 CGGTGTTCGATTGACCAATGATTCGCGGGAAGGGA 74

RESULT 10
ID PCT-US95-11869-1 STANDARD; DNA; UNC; 1809 BP.
AC xxxxxx
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```

DE Sequence 1, Application PC/TUS9511869
DE Sequence 1, Application PC/TUS9511869
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
CC TITLE OF INVENTION: Thereto
CC NUMBER OF SEQUENCES: 5
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE:
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11869
CC FILING DATE: 19-SEP-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Vincant, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: HMI-011CPCPC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 227-7400
CC TELEFAX: (617) 227-5941
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1809 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: both
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 265..891
CC FEATURE:
CC NAME/KEY: 5'UTR
CC LOCATION: 1..264
CC FEATURE:
CC NAME/KEY: 3'UTR
CC LOCATION: 892..1809
CC FEATURE:
CC NAME/KEY: sig_peptide
CC LOCATION: 255..324
CC SEQUENCE 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 OTHER.
SQ

Query Match 0.68; Score 36; DB 2; Length 1809;
Best Local Similarity 80.0%; Pred. No. 1.83e-07;
Matches 48; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 260 GGGCATGGCGCGCGCGCGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 319
Cp 6335 GGGACTTCCGCGCTGCTGCTGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 6276

RESULT 11
ID US-07-745-206A-6 STANDARD; DNA; UNC; 5904 BP.
AC xxxxxx

DE Sequence 6, Application US/07745206A
DE Sequence 6, Application US/07745206A
CC Patent No. 5429921
CC GENERAL INFORMATION:
CC APPLICANT: Harpold, Michael
CC APPLICANT: Ellis, Steven
CC APPLICANT: Williams, Mark
CC APPLICANT: McCue, Ann
CC APPLICANT: Feldman, Daniel
CC TITLE OF INVENTION: Human Calcium Channel Compositions and
CC TITLE OF INVENTION: Methods
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fitch, Even, Tabin & Flannery
CC STREET: 135 S. LaSalle
CC CITY: Chicago
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STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/745,206A  
FILING DATE: 19910815  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-372-7842  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5904 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE 5904 bp: 1353 A: 1717 C: 1544 G: 1260 T: 30

Query Match	0.68;	Score 39;	DB 1;	Length 5904;
Best Local Similarity	60.3%;	Pred. No. 2.69e-09;		
Matches 114;	Conservative 75;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	2504	CATTGTGCTCAACACGATGTTCAATGGCAATGGATCACCAAGATATGAACAAGAGATGGA	2563	
Db	3819	AATGGCCATGAACATCTCAACATGCTTCTACTGGCCTCTTACCCTGGAGATGATCCT	3878	
QY	2564	ACGGCTGCTCAAGAGTGGCAACTATTTCTTACCGCCACCTTTGGCCATCGAGGCCACCAT	2623	
Db	3879	GAAGCTCATTCCTTCAACCCCAAGGGTTACTTAGTGATCCCTGGAAATGTTTTTGACTT	3938	
QY	2624	GAAGCTAATGGCCATGAGCCCAAGTACTATTTCCAGGAGGGCTGGAACTCTTCGACTT	2683	
Db	3939	CCTCATCGT	3947	
QY	2684	CATTATCGT	2692	

RESULT 12  
 ID 5386025-5 STANDARD; DNA; UNC; 6459 BP.  
 AC xxxxxx  
 DT 01-JAN-1900  
 DE Patent No. 5386025.  
 CC Patent No. 5386025  
 CC APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL.  
 CC M.: CAMPBELL, KEVIN P.  
 CC TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS  
 CC NUMBER OF SEQUENCES: 9  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/482,384  
 CC FILING DATE: 20-FEB-1990  
 CC SEQ ID NO:5:  
 CC LENGTH: 5962  
 CC Sequence 6459 BP; 1280 A; 1835 C; 1691 G; 1156 T; 497 other;

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Qy	5247	CTGTGGAAGGAGGCAAGGGCATTCGGACATCGCTCTTCGCTTGGGCATTCGCTGCC	5306			
Db	3922	GCCCTGCGCCTACGTGGCGCCCTGCTCATCGTCAATGCTGTTCTTTCATCTACGCCGCTCATCGC	3981			

QY	5307	GCCTGTTCACATCGCCTGCTGCTTCCCTGGTCAATTGTTTCATCTTTSCCATTTTCGCC	5366
Dd	3982	ATG 3984	
QY	5367	ATG 5369	
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ID	US-08-336-257A-3	STANDARD; DNA; UNC; 5975 BP.	
AC	xxxxxx		
DT			
DE	Sequence 3,	Application US/08336257A	
CC	Sequence 3,	Application US/08336257A	
CC	Patent No.	5726035	
CC	GENERAL INFORMATION:		
CC	APPLICANT:	Jay, Scott D	
CC	APPLICANT:	Ellis, Steven B.	
CC	APPLICANT:	Harpold, Michael M.	
CC	APPLICANT:	Campbell, Kevin P.	
CC	TITLE OF INVENTION:	CALCIUM CHANNEL COMPOSITIONS AND METHODS	
CC	NUMBER OF SEQUENCES:	8	
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE:	Brown, Martin, Haller & McClain	
CC	STREET:	1660 Union Street	
CC	CITY:	San Diego	

RESULT	13	
ID	US-08-336-257A-3	STANDARD; DNA; UNC; 5975 BP.
AC	xxxxxx	
DT		
DE	Sequence 3,	Application US/08336257A
CC	Sequence 3,	Application US/08336257A
CC	Patent No. 5726035	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	Jay, Scott D
CC	APPLICANT:	Ellis, Steven B.
CC	APPLICANT:	Harpold, Michael M.
CC	APPLICANT:	Campbell, Kevin P.
CC	TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS	
CC	NUMBER OF SEQUENCES:	8
CC	CORRESPONDENCE ADDRESS:	
CC		

C111: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/336,257A  
 FILING DATE: 07-NOV-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 54898  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 238-0999  
 TELEFAX: (619) 238-0062  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5975 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: Genomic DNA  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 79...5700  
 OTHER INFORMATION: \product= "Alpha-1 subunit of animal calcium  
 OTHER INFORMATION: channel"  
 SEQUENCE 5975 BP; 1291 A; 1832 C; 1694 G; 1158 T; 0 OTHER.

Query Match	0.6%	Score 37	DB 1	Length 5975
Best Local Similarity	65.0%	Pred. No. 4.54e-08		
Matches	80	Conservative	0	Mismatches 43
			Indels	0
			Gaps	0
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Qy	5247	CTGTGTGAGGAGGCCAAGGGCATCTGGACACTGCTTCCGTTGCCCATGTGCGTGC	5306	
Db	3874	GCCCTGCCCCACGTGGCGCCCTGCTCATGTCATGTCATCTACGCGGTCATCGC	3933	
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Query Match      0.6%; Score 37; DB 1; Length 5975;
Best Local Similarity 65.0%; Pred. No. 4.54e-08;
Matches 80; Conservative 43; Mismatches 43; Indels 0; Gaps 0;

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v 5247 CTGCTGAGGGGAGCCAAAGGCATTTCGACATCTGCTCTTCGGCTTGGCGATTCGCTGCCG 5306
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	Db	3814	CTGCTGAGTCGGGCCGAGGGCGTGCACAGCTGCTGTGGACGTTATCAAGTCCTTCCAG	3873
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Wed Jul 8 10:16

Db 3874 GCCCTGC  
Qy 5307  
Db 3934  
Qy 5362

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Jul 8 01:51:13 1998; MasPar time 4842.76 Seconds  
Tabular output not generated. 1208.554 Million cell updates/sec

Title: >US-08-554-424-7  
Description: (1-6513) from US08554424.seq  
Perfect Score: 6513

N.A. Sequence: 1 TCTAGACGTTGCCGCATAG.....ACGCGAGTATTAGCTCTAGA 6513  
Comp: AGATCTGCAACGGCGGTATC.....TGGCGCTAATACGAGATCT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1384628 seqs, 449312139 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-pending

1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005  
8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82  
15:U83 16:U84A 17:U84B 18:U85 19:U86 20:U87 21:U88  
22:U89 23:U90A 24:U90B 25:U91 26:NEWU8

Statistics: Mean 11.817; Variance 4.148; scale 2.848

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	18	US-08-554- Sequence 7, Applicatio	0.00e+00
2	5500	84.4	6519	21	US-08-808- Sequence 24, Applicati	0.00e+00
3	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
4	4374	67.2	5461	11	US-07-998- Sequence 7, Applicatio	0.00e+00
5	3676	56.4	6318	1	PCT-US97-2 Sequence 1, Applicatio	0.00e+00
6	3676	56.4	6318	21	US-08-808- Sequence 1, Applicatio	0.00e+00
7	3664	56.3	6315	1	PCT-US97-2 Sequence 2, Applicatio	0.00e+00
8	3664	56.3	6315	21	US-08-808- Sequence 2, Applicatio	0.00e+00
9	3662	56.2	6318	19	US-08-608- Sequence 1, Applicatio	0.00e+00
10	3660	56.2	6318	19	US-08-608- Sequence 2, Applicatio	0.00e+00
11	472	7.2	1237	21	US-08-808- Sequence 26, Applicati	0.00e+00
12	356	5.5	5977	23	US-09-024- Sequence 1, Applicatio	0.00e+00
13	356	5.5	6007	23	US-09-024- Sequence 2, Applicatio	0.00e+00
14	356	5.5	6556	23	US-09-024- Sequence 7, Applicatio	0.00e+00
15	354	5.4	6826	23	US-09-024- Sequence 8, Applicatio	0.00e+00
16	320	4.9	6048	19	US-08-682- Sequence 1, Applicatio	0.00e+00
17	316	4.9	6452	21	US-08-836- Sequence 9, Applicatio	0.00e+00

18	312	4.8	3033	15	US-08-334- Sequence 1, Applicatio	0.00e+00
19	312	4.8	3033	21	US-08-336- Sequence 1, Applicatio	0.00e+00
20	308	4.7	6371	21	US-08-836- Sequence 13, Applicati	0.00e+00
21	308	4.7	6404	21	US-08-836- Sequence 14, Applicati	0.00e+00
22	298	4.6	6344	18	US-08-511- Sequence 1, Applicatio	0.00e+00
23	298	4.6	6344	21	US-08-843- Sequence 1, Applicatio	0.00e+00
24	296	4.5	6524	20	US-08-775- Sequence 1, Applicatio	2.65e-301
25	296	4.5	6524	19	US-08-669- Sequence 1, Applicatio	2.65e-301
26	296	4.5	6527	20	US-08-775- Sequence 7, Applicatio	2.65e-301
27	296	4.5	6527	19	US-08-669- Sequence 7, Applicatio	2.65e-301
28	296	4.5	7052	19	US-08-669- Sequence 5, Applicatio	2.65e-301
29	296	4.5	7052	20	US-08-775- Sequence 5, Applicatio	2.65e-301
30	254	3.9	5874	21	US-08-843- Sequence 9, Applicatio	1.63e-231
31	231	3.5	2573	20	US-08-775- Sequence 3, Applicatio	2.09e-224
32	231	3.5	2573	19	US-08-669- Sequence 3, Applicatio	2.09e-224
33	214	3.3	930	19	US-08-605- Sequence 2, Applicatio	1.86e-204
34	204	3.1	930	19	US-08-605- Sequence 21, Applicati	9.16e-193
35	194	3.0	930	19	US-08-605- Sequence 3, Applicatio	4.18e-181
36	192	2.9	930	19	US-08-605- Sequence 3, Applicatio	8.89e-179
37	177	2.7	2279	11	US-07-998- Sequence 1, Applicatio	2.26e-161
38	177	2.7	2279	11	US-07-998- Sequence 3, Applicatio	2.26e-161
39	171	2.6	696	23	US-09-024- Sequence 5, Applicatio	1.94e-154
40	148	2.3	5482	15	US-08-346- Sequence 2, Applicatio	4.97e-128
41	134	2.1	702	18	US-08-511- Sequence 3, Applicatio	4.07e-112
42	134	2.1	702	21	US-08-843- Sequence 3, Applicatio	4.07e-112
43	119	1.8	5389	15	US-08-346- Sequence 1, Applicatio	3.07e-95
44	110	1.7	7218	17	US-08-466- Sequence 14, Applicati	3.23e-85
45	103	1.6	568	11	US-07-998- Sequence 10, Applicati	1.74e-77

ALIGNMENTS

RESULT 1  
ID US-08-554-424-7 STANDARD; DNA; UNC; 6513 BP.  
AC xxxxxx  
DE Sequence 7, Application US/08554424  
CC Sequence 7, Application US/08554424  
CC GENERAL INFORMATION:  
CC APPLICANT: Warmke, Jeffrey W.  
CC APPLICANT: Van Der Ploeg, Leonardus  
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
CC TITLE OF INVENTION: PARA SODIUM CHANNEL  
CC NUMBER OF SEQUENCES: 7  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Jack L. Tribble  
CC STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CC CITY: Rahway  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 07065-0907  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/554,424  
CC FILING DATE:  
CC CLASSIFICATION: 424  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Tribble, Jack L.  
CC REGISTRATION NUMBER: 32,633  
CC REFERENCE/DOCKET NUMBER: 19338DA  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (908) 594-5321  
CC TELEFAX: (908) 594-4720  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6513 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear

CC	MOLECULE TYPE: cDNA	
SQ	SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.	
	Query Match 100.0%; Score 6513; DB 18; Length 6513;	
	Best Local Similarity 100.0%; Pred. No. 0.00e+00;	
	Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 TCTAGAGCTTTGGCCGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAGAAC 60	961 ATCTGACCGACGAGAACTGGGACTATACAAATCGCAATAGTCCAAATGGTATTCGAGG 1020
QY	1 TCTAGAGCTTTGGCCGATAGACAATGACAGAAGATTCGGACTCGATATCTGAGGAGAAC 60	
Db	61 GCAGTTTTCCTCCCTTTACCGCGCAATCATTTGGTGAATCGAACACGCAATTCGCG 120	1021 ACAGGGCATCTCATTTCCGTTATCGGCAATATATCCGGTCGGGGCAATGCGAGACG 1080
QY	61 GCAGTTTTCCTCCCTTTACCGCGCAATCATTTGGTGAATCGAACACGCAATTCGCG 120	
Db	121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAGAGAGCCGAGGAGAGGTCCCGCAT 180	1081 ATTACGTGTGCTCGACAGGGTTTGGTCCGAATCCGAATATGCGTACACAGCTTCGATT 1140
QY	121 CTGAACATGAAAGCAGAGAGAGCTGGAAGAGAGAGCCGAGGAGAGGTCCCGCAT 180	
Db	181 ATGTCGCAAGAAAACAAAGAAATCCGATATGATGACGAGGAGAGATGAAGGTC 240	1141 CGTTCCGATGGCTTTCCTGTCGCCCTTCGGCTGATGACACAGGACTTCTGGGAGATC 1200
QY	181 ATGTCGCAAGAAAACAAAGAAATCCGATATGATGACGAGGAGAGATGAAGGTC 240	
Db	241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTTCAGGGCAGCT 300	1201 TGTACACGTGCTGTGTCGCCGCCCGACCATGGCACATGCTGCTTTTATAGTCATCA 1260
QY	241 CACAACCGGATCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTTCAGGGCAGCT 300	
Db	301 TCCCGCCGGAATGGCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360	1261 TGTACACGTGCTGTGTCGCCGCCCGACCATGGCACATGCTGCTTTTATAGTCATCA 1260
QY	301 TCCCGCCGGAATGGCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360	
Db	361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGTTTCTGCAATCAAAAGCAA 420	1320 TCTTCTTAGTTCATTTCTTGTGAATTTGATTTGGCCATTTGGCCATTTGTCGATG 1320
QY	361 TGACATTCGTAGTTGTAAGCAAGAAAGAAATATTTTCGTTTCTGCAATCAAAAGCAA 420	
Db	421 TGTGATGCTGCATCCATCAATCCGATACGTCGTTGGTGGCCATTTACATTCAGTGATC 480	1320 TCTTCTTAGTTCATTTCTTGTGAATTTGATTTGGCCATTTGGCCATTTGTCGATG 1320
QY	421 TGTGATGCTGCATCCATCAATCCGATACGTCGTTGGTGGCCATTTACATTCAGTGATC 480	
Db	481 CATTAATTTCCCTATTCATCATCACCAATCTCGTCAACTGATCTGATGATATGTC 540	1380 ACGAATTCGAAGGAAGGCCGAAGAAAGAGGCTGCCGAAGAGAGGCGGATACGTGAAG 1380
QY	481 CATTAATTTCCCTATTCATCATCACCAATCTCGTCAACTGATCTGATGATATGTC 540	
Db	541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACATTTGAAT 600	1380 ACGAATTCGAAGGAAGGCCGAAGAAAGAGGCTGCCGAAGAGAGGCGGATACGTGAAG 1380
QY	541 CGACAACGCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACATTTGAAT 600	
Db	601 CAGCTGTTAAAGTGATGGCACGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660	1440 CGGAAGAAGCTGCCGCCGCCAAAGCGCCAAAGCTGGAGAGCGGGCCAAATCGCAGGCTC 1440
QY	601 CAGCTGTTAAAGTGATGGCACGAGTTTCATTTTATGCCGTTTACGTATCTTAGAGATG 660	
Db	661 CATGGAAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720	1441 AGGACAGCAGCGATCGGCTGCCGCCGAAGAGGCTGCATCGCAATCCGGAATGGCCAAGA 1500
QY	661 CATGGAAATGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720	
Db	721 TAGGTAAATCTAGCAGCCCTCGCAACGTTTGGGTGCTGGAGCGCTTAAACCGTAGCCA 780	1500 GTCCGACGTTATTTTGCATCAGCTATGAGCTATTTGTTGGCGGCGAGAAGGCGCAACGATG 1560
QY	721 TAGGTAAATCTAGCAGCCCTCGCAACGTTTGGGTGCTGGAGCGCTTAAACCGTAGCCA 780	
Db	781 TTGTGCCAGGCTTGAGACCATCTGCGCGCGTCAATCGAATCGGTGAAGAATCTGCGCG 840	1561 ACACAAACAAAGAGAAGATGTCCTATCGGAGCGTCGAGGTGGAGTCGGGTGAGCG 1620
QY	781 TTGTGCCAGGCTTGAGACCATCTGCGCGCGTCAATCGAATCGGTGAAGAATCTGCGCG 840	
Db	841 ATGTGATTATCTGACCATGTTCTCCCTGTGCGGTGTTCCGGTTGATGGCCCTACAGATCT 900	1620 ACACAAACAAAGAGAAGATGTCCTATCGGAGCGTCGAGGTGGAGTCGGGTGAGCG 1620
QY	841 ATGTGATTATCTGACCATGTTCTCCCTGTGCGGTGTTCCGGTTGATGGCCCTACAGATCT 900	
Db	901 ATATGGCGGTGCTACCGAGAAGTGATCAAGAAAGTTCCCGCTGGACGGTTCTTGGGCA 960	1680 TATACAAAGACAACACAGCACCTTACACAGCACACCAAGCTACCAAAAGTTCGTAAGTGA 1680
QY	901 ATATGGCGGTGCTACCGAGAAGTGATCAAGAAAGTTCCCGCTGGACGGTTCTTGGGCA 960	
Db	961 ATCTGACCGACGAGAACTGGGACTATCACAAATCGCAATAGTCCAAATGGTATTCGAGG 1020	1681 GCACGACATCTTATCTTACCTGTTACCGTTTAAACATACGACAGGGATCACGTAGTT 1740
QY	961 ATCTGACCGACGAGAACTGGGACTATCACAAATCGCAATAGTCCAAATGGTATTCGAGG 1020	



Db 2101 CCTGCTCGACACCAATCACAAAGCTCGATCATCGGACTACGAATTTGGCCCTGGAGTGCA 2160  
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|  
Qy 2101 CCTGCTCGGACCAATCACAAAGCTCGATCATCGGACTACGAATTTGGCCCTGGAGTGCA 2160  
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Db 2161 CGGAGAGCTGGCAAGATTAAACATCATGACATCCCTTTTATCGAGCCCTCCAGACAC 2220  
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|  
Qy 2161 CGGAGAGCTGGCAAGATTAAACATCATGACATCCCTTTTATCGAGCCCTCCAGACAC 2220  
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Db 2221 AAACGGTGGTATGATGAAAGATGTGATGGTCTGCTGAATGACATCATCGAACAGGCCGCTG 2280  
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|  
Qy 2221 AAACGGTGGTATGATGAAAGATGTGATGGTCTGCTGAATGACATCATCGAACAGGCCGCTG 2280  
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Db 2281 GTCGACAGCTGGGCAAGCATCGCGGTGTCCTCGTTTACTATTTCCTCCACAGAGGACG 2340  
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Qy 2281 GTCGACAGCTGGGCAAGCATCGCGGTGTCCTCGTTTACTATTTCCTCCACAGAGGACG 2340  
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Db 2341 ATGACGAGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCTCAAAGGCATCG 2400  
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Qy 2341 ATGACGAGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCTCAAAGGCATCG 2400  
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Db 2401 ATGTGTTTTGTGTGGGACTGTGCTGGGTTGGTTGAAATTTTCAGAGTGGGTATCGC 2460  
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Qy 2401 ATGTGTTTTGTGTGGGACTGTGCTGGGTTGGTTGAAATTTTCAGAGTGGGTATCGC 2460  
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Db 2461 TCATCGTCTTGATCCCTTCGTGAGCTTCTCATCACGCTGTGCATGAGTGTGTCACACGA 2520  
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Qy 2461 TCATCGTCTTGATCCCTTCGTGAGCTTCTCATCACGCTGTGCATGAGTGTGTCACACGA 2520  
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Db 2521 TGTTTCATGCAATGATCACACGATATGAACAAGGACATGGAAGCGTGTCTCAAGAGTG 2580  
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Qy 2521 TGTTTCATGCAATGATCACACGATATGAACAAGGACATGGAAGCGTGTCTCAAGAGTG 2580  
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Db 2581 GCAACTATTTCTCACCCGACCTTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
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Qy 2581 GCAACTATTTCTCACCGCACCTTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2640  
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Db 2641 GCCCAAGTACTATTTCAGAGAGGCTGGAACATCTTCGACTTCATATTCGTGGCCCTAT 2700  
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Qy 2641 GCCCAAGTACTATTTCAGAGAGGCTGGAACATCTTCGACTTCATATTCGTGGCCCTAT 2700  
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Db 2701 CGCTATTGGAAGTGGACTCGAGGGTGTCCAGGGTCTCTCGGTATGCGTTCCTTCGAT 2760  
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Qy 2701 CGCTATTGGAAGTGGACTCGAGGGTGTCCAGGGTCTCTCGGTATGCGTTCCTTCGAT 2760  
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Db 2761 TGCTCGGTGATTTCAAAGTGGCCAAAGTCTTGCCGACACACTTAATTTACTCATTTTCGATTA 2820  
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Db 2821 TGGGACGACCATGGCGCTTTGGGTAAATCTGACATTTGTACTTTGCAATTCATCTTCA 2880  
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Qy 2821 TGGGACGACCATGGCGCTTTGGGTAAATCTGACATTTGTACTTTGCAATTCATCTTCA 2880  
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Db 2881 TCTTTGCGGTGATGGGATGCAACTGTTGCGAAGAAATATCATGATCACAGGACCCT 2940  
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Qy 2881 TCTTTGCGGTGATGGGATGCAACTGTTGCGAAGAAATATCATGATCACAGGACCCT 2940  
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Db 2941 TTCGGAATGGGACCTGCGCGCTGGAAGTCTCACCGACTTTATGACAGACTTCATGATCG 3000  
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Db 3001 TGTTCGCGGTGCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCAATGACGTGGCGG 3060  
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Qy 3001 TGTTCGCGGTGCTGCGGAGAAATGGATCGAGTCCATGTGGGACTGCAATGACGTGGCGG 3060  
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Db 3061 ATGTCTCGTGCATTCCTTCTCTTGGCCACCGTGTGTCATCGGCAATCTGTGGTACTTA 3120  
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Qy 3061 ATGTCTCGTGCATTCCTTCTCTTGGCCACCGTGTGTCATCGGCAATCTGTGGTACTTA 3120  
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Db 3121 ACCTTTCTTACCTTGTCTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG 3180  
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Qy 3121 ACCTTTCTTACCTTGTCTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG 3180  
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Db 3181 CCGATAACGATACGAATAAAATAGCCGAGGCTTCAATCGAATTTGGCGGATTTAAAGTT 3240  
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Qy 3181 CCGATAACGATACGAATAAAATAGCCGAGGCTTCAATCGAATTTGGCGGATTTAAAGTT 3240  
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Db 3241 GGGTTAAGCGTAATATTGCTGATTGTTTCAAGTTAATACGTTAAACAAATTTGACAAATCAA 3300  
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Qy 3241 GGGTTAAGCGTAATATTGCTGATTGTTTCAAGTTAATACGTTAAACAAATTTGACAAATCAA 3300  
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Db 3301 TAACTGATCAACCATCAAGTGTGAGAGGACCACCAAGATCAGTTGGATTGGAGCGAAGAGC 3360  
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Qy 3301 TAACTGATCAACCATCAAGTGTGAGAGGACCACCAAGATCAGTTGGATTGGAGCGAAGAGC 3360  
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Db 3361 ATGCTGACAGAACTGGAGCTGGGCCACGACGAGATCTCTCGCGAGCGCCCTCATCAAGA 3420  
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Qy 3421 AGGGATCAAGGACGACAGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3480  
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Db 3481 TACACGGCGACATGAAGAACAACAAAGCCGGAAGAAATCCAAATATCTAAATTAACCAACGA 3540  
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Qy 3481 TACACGGCGACATGAAGAACAACAAAGCCGGAAGAAATCCAAATATCTAAATTAACCAACGA 3540  
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Db 3541 TGATTGGCACTCAATTAACCAACCAAGACTAGACTGGAAACAGAGCTAAACCATAGAG 3600  
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Qy 3541 TGATTGGCACTCAATTAACCAACCAAGACTAGACTGGAAACAGAGCTAAACCATAGAG 3600  
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Db 3601 GTTTGTCTTACAGGACGACACACTGCCAGCATTAATCTATATGTTAGCCATAGAATC 3660  
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Qy 3601 GTTTGTCTTACAGGACGACACACTGCCAGCATTAATCTATATGTTAGCCATAGAATC 3660  
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Db 3661 GACCATTCAAGGACGAGGCCACAAAGGCGACGCCGAGACGATGGAGGCGGAGGAGAGC 3720  
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Db 3721 GCGAGCCGACCAAGAGGATTTAGTCTCGAGAGGAACTGGAGAGGAGGCGGAAATCGG 3780  
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Qy 3721 GCGAGCCGACCAAGAGGATTTAGTCTCGAGAGGAACTGGAGAGGAGGCGGAAATCGG 3780  
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Db 3781 AGGAGGCCGCTCGAGGCTGATATCATTTATGACACGACGAGGATATCTCGATG 3840  
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Qy 3781 AGGAGGCCGCTCGAGGCTGATATCATTTATGACACGACGAGGATATCTCGATG 3840  
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Db 3841 AATATCCAGCTGATTGCTGCCCGATTCTGTACTATAGAAATTTCCGATCTTAGCCGCTG 3900  
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Qy 3841 AATATCCAGCTGATTGCTGCCCGATTCTGTACTATAGAAATTTCCGATCTTAGCCGCTG 3900  
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Db 3901 ACATGACTCGCGCTTCTGCAAGGATGGGGCAATTTACGACTGAAACTTTTCAATTA 3960  
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Qy 3901 ACATGACTCGCGCTTCTGCAAGGATGGGGCAATTTACGACTGAAACTTTTCAATTA 3960  
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Db 3961 TTGAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTATGATGAGTACTGCTT 4020  
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Qy 3961 TTGAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTATGATGAGTACTGCTT 4020  
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Db 4021 TGGCATTAGAAAGATGATACATCTGCCAAAGACCCATCTCAGGATATTTTACTATA 4080  
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Qy 4081 TGGACAGAAATTTACGGTTATATCTCTTGGAAATTTAATCAAGTGGTGGCGCTCG 4140  
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Db 4141 GCTTCAAGTCTACTTCAACCAAGCGTGTGTTGGCTCGATTTCTGATTTCTATGTTAT 4200  
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Qy 4141 GCTTCAAGTCTACTTCAACCAAGCGTGTGTTGGCTCGATTTCTGATTTCTATGTTAT 4200  
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Db 4201 CGCTTATCAACTTCTGTTCTTCACTTGTGAGCTGGTGGTATTCAAGCCTTTCAAGACTA 4260  
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Qy 4201 CGCTTATCAACTTCTGTTCTTCACTTGTGAGCTGGTGGTATTCAAGCCTTTCAAGACTA 4260  
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|  
Db 4261 TCGAAGCTTAAAGCACTGAGACCACCTACGTGCCATGTCCCGTATGCGAGGCGACTG 4320  
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D	b	1261	GTGAATTTGATTTTGGCCATTGTCGCAATCTCGTATGACGAATTGC	AAGAAAGCCGAA	1320
Q	y	1284	GTGAATTTGATTTTGGCCATTGTCGCAATCTCGTATGACGAATTGC	AAGAAAGCCGAA	1343
D	b	1321	GAAGAAGAGCTGCCGAAGAGGCGGATACGTTAAGCGGAAGAAGCT	TGCCGCGCCAA	1380
Q	y	1344	GAAGAAGAGCTGCCGAAGAGGCGGATACGTTAAGCGGAAGAAGCT	TGCCGCGCCAA	1403
D	b	1381	CGCGCCAAAGCTGGAGGAGCGGGCCAAATGCCAGGCTCAGCAGCGAT	CGCGGTGCTGCC	1440
Q	y	1404	CGCGCCAAAGCTGGAGGAGCGGGCCAAATGCCAGGCTCAGCAGCGAT	CGCGGTGCTGCC	1463
D	b	1441	GCCGAAGAGGCTGCACATGCAATCCGGAATGCCAAGAGTCCGAGCTAT	CTTGATCAGC	1500
Q	y	1464	GCCGAAGAGGCTGCACATGCAATCCGGAATGCCAAGAGTCCGAGCTAT	CTTGATCAGC	1523
D	b	1501	TATGAGCTATTTGTGGCGGCGAAGGGCAACCATGACACACAAAGAGA	GATGCTGC	1560
Q	y	1524	TATGAGCTATTTGTGGCGGCGAAGGGCAACCATGACACACAAAGAGA	GATGCTGC	1583
D	b	1561	ATTGCGAGCGTCGAGTGGAGTCGGAGTCGGTGAGCGCTTATACAAAG	ACACACGACCT	1620
Q	y	1584	ATTGCGAGCGTCGAGTGGAGTCGGAGTCGGTGAGCGCTTATACAAAG	ACACACGACCT	1643
D	b	1621	ACCACAGCACACCAAGCTACCAAAAGTCGTTAAAGTAGCAGCAGCAT	CTTATCCTTACCT	1680
Q	y	1644	ACCACAGCACACCAAGCTACCAAAAGTCGTTAAAGTAGCAGCAGCAT	CTTATCCTTACCT	1703
D	b	1681	GTTTCACCGTTTAAACATACGAGGGGGATCAGTAGTCTCTCAAAGT	ACACGATACGGAAC	1740
Q	y	1704	GTTTCACCGTTTAAACATACGAGGGGGATCAGTAGTCTCTCAAAGT	ACACGATACGGAAC	1763
D	b	1741	GGAGCTGGCGCGTTTGGTATACCCGGTAGCGATCTAGCCATTTGGTAT	TGTACACATAT	1800
Q	y	1764	GGAGCTGGCGCGTTTGGTATACCCGGTAGCGATCTAGCCATTTGGTAT	TGTACACATAT	1823
D	b	1801	CAGGATGCCCGCAGCAGCTTCCCTATGCCGAGACTCGAATGCCGT	CACCCCGATGCC	1860
Q	y	1824	CAGGATGCCCGCAGCAGCTTCCCTATGCCGAGACTCGAATGCCGT	CACCCCGATGCC	1883
D	b	1861	GAAGAGAATGGGGCCATCATAGTGCCTGTACTATGGCAATCTAGGCT	TCGACACTCA	1920
Q	y	1884	GAAGAGAATGGGGCCATCATAGTGCCTGTACTATGGCAATCTAGGCT	TCGACACTCA	1943
D	b	1921	TGCTATACCTCGCATCAGTCGCGAATATCGTACTCTACATGGCGAT	CTACTCGCGCGC	1980
Q	y	1944	TGCTATACCTCGCATCAGTCGCGAATATCGTACTCTACATGGCGAT	CTACTCGCGCGC	2003
D	b	1981	ATGGCGCTCATGGCGCTCAGCACAATGACCAAGGAGAGCAAAATGG	CGCAACCGCAACCA	2040
Q	y	2004	ATGGCGCTCATGGCGCTCAGCACAATGACCAAGGAGAGCAAAATGG	CGCAACCGCAACCA	2063
D	b	2041	CGCAATCAATCAGTGGGCGCCACCAATGGGGCACCACCTGCTTGAC	ACCACCAATCACAG	2100
Q	y	2064	CGCAATCAATCAGTGGGCGCCACCAATGGGGCACCACCTGCTTGAC	ACCACCAATCACAG	2123
D	b	2101	CTCGATCATCGCACTACGAAATTTGGCCTGGAGTCGACGACGAACT	GGCAAGATTTAA	2160
Q	y	2124	CTCGATCATCGCACTACGAAATTTGGCCTGGAGTCGACGACGAACT	GGCAAGATTTAA	2183
D	b	2161	CATCATGACAAATCCTTTTATCGAGCGGCTCCAGACACAAACGTT	GTTGATTAAGAT	2220
Q	y	2184	CATCATGACAAATCCTTTTATCGAGCGGCTCCAGACACAAACGTT	GTTGATTAAGAT	2243
D	b	2221	GTGATGCTCTGTAATGATCATCTCGAACAGGCGCGTGGTCGGCAC	AGTCGGGCAACCGAT	2280
Q	y	2244	GTGATGCTCTGTAATGATCATCTCGAACAGGCGCGTGGTCGGCAC	AGTCGGGCAACCGAT	2303
D	b	2281	CGCGGTG-----AGACGATGACGAGATGGCGCGACGTTTC		2316
Q	y	2304	CGCGGTGCTCTCCGTTTACTATTTCCCAACAGAGACGATGACGAG	GATGGCGCGACGTTTC	2363
D	b	2317	NAACACACAGCTCTCGAGTGATCTCTCAAAGGCATCGATGTTTGT	TGTGTGGGACTGT	2376

QY	2364	AAAGACAAAGGCACCTCGAAGTGA	CTCTCAAGAGCATCGAATGTTTGTCTGGGACTGT	2423
Db	2377	TGCTGGGTTCGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGTC	2436	
QY	2424	TGCTGGGTTCGGTTGAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGTC	2483	
Db	2437	GAGCTCTTCATCACGCTGTGCATTTGTGTCAACACAGATGTTTCATGGCAATGGATCACCAC	2496	
QY	2484	GAGCTCTTCATCACGCTGTGCATTTGTGTCAACACAGATGTTTCATGGCAATGGATCACCAC	2543	
Db	2497	GATATGAACAAGAGATGAACGCGTGTCAAGAGTGGCAACTATTTCTTCACCGCCACC	2556	
QY	2544	GATATGAACAAGAGATGAACGCGTGTCAAGAGTGGCAACTATTTCTTCACCGCCACC	2603	
Db	2557	TTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAGGAG	2616	
QY	2604	TTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAGGAG	2663	
Db	2617	GGGTGAAACATCTTCACATTCATTATCGTGGCCATCGCTATTTGGAATGGGACTCGAG	2676	
QY	2664	GGGTGAAACATCTTCACATTCATTATCGTGGCCCTATCCCTATTTGGAATGGGACTCGAG	2723	
Db	2677	GGTGTCCAGGGTCTGTCCGTATTCGCTTCCTTTTCGATTCGCTGCTATTCAACTGGCC	2736	
QY	2724	GGTGTCCAGGGTCTGTCCGTATTCGCTTCCTTTTCGATTCGCTGCTATTCAACTGGCC	2783	
Db	2737	AACTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTATGGGAGCGCACCATGGCGCTTGG	2796	
QY	2784	AACTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTATGGGAGCGCACCATGGCGCTTGG	2843	
Db	2797	GGTAATCTGACATTTGTACTTTTCGATTTATCATCTTTCGCGTGTATGGGAATGCAA	2856	
QY	2844	GGTAATCTGACATTTGTACTTTTCGATTTATCATCTTTCGCGTGTATGGGAATGCAA	2903	
Db	2857	CTGTTCGGAAGAATTAATCATGATCAAGGACCGCTTTCCGATGGCGACCTGCCGCGC	2916	
QY	2904	CTGTTCGGAAGAATTAATCATGATCAAGGACCGCTTTCCGATGGCGACCTGCCGCGC	2963	
Db	2917	TGGAACCTTACCAGCTTTATGCACAGCTTCATGATCGTGTTCGGGTGCTCGCGAGAA	2976	
QY	2964	TGGAACCTTACCAGCTTTATGCACAGCTTCATGATCGTGTTCGGGTGCTCGCGAGAA	3023	
Db	2977	TGGATCGAGTCCATGTGGGACTGCGATGCTGTGGCGATGCTGTGCGATTCCTTCTTC	3036	
QY	3024	TGGATCGAGTCCATGTGGGACTGCGATGCTGTGGCGATGCTGTGCGATTCCTTCTTC	3083	
Db	3037	TTGGCCACCGTTGCTATCGGCAATCTTGTGGTACTTAACCTTTTCTTAGCCTTCCTTTTG	3096	
QY	3084	TTGGCCACCGTTGCTATCGGCAATCTTGTGGTACTTAACCTTTTCTTAGCCTTCCTTTTG	3143	
Db	3097	TCCAATTTTGCTCATCTAGCTTATCAGCGCGACTCCGCGATAACGATACGAATAAATA	3156	
QY	3144	TCCAATTTTGCTCATCTAGCTTATCAGCGCGACTCCGCGATAACGATACGAATAAATA	3203	
Db	3157	GCCGAGGCCTTCAATTCGAAATTTGGCGGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT	3216	
QY	3204	GCCGAGGCCTTCAATTCGAAATTTGGCGGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT	3263	
Db	3217	TGTTTCAAGTTAATACGTAAACAAATTTGACAATCAAAATACGTATCAACCATCAG	3271	
QY	3264	TGTTTCAAGTTAATACGTAAACAAATTTGACAATCAAAATACGTATCAACCATCAG	3322	
Db	3272	-----AGCATGTGTACAACGACTGGAGCTG	3291	
QY	3324	AGGACCAACCGATCAGTTGGATTTGGAGCGAAGAGCATGTTGACAACGACTGGAGCTG	3388	
Db	3298	GGCCACGAGGATCCTGCGCAGCGCTCATCAGAGGGGATCAAGAGCAGACGAA	3355	
QY	3384	GGCCACGAGGATCCTGCGCAGCGCTCATCAGAGAGGGGATCAAGAGCAGACGAA	3441	
Db	3358	CTGGAGTGGCCATCGGGATGGCAATTCAGATACACGGCGACATGAAGAACAC	3411	

QY 3444 CTGAGGTGCCATCGGGATCGGATGGAATTACAGATACACGGCGACATGAAGACAAC 3503  
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QY 3504 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGTTGCAACTCAATTAACCAAC 3563  
Db 3454 -----GAGCAGCAG 3462  
QY 3564 CAAGACAATAGACTGGAAACACGAGCTAAACCATAGAGGTTTGCCTTACAGGACGAGCAG 3623  
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QY 3624 ACTGCCAGCATTAACATCATATGTTAGCCATAAGAAATCGACCATTCGAAGCAGGAGGCCAC 3683  
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QY 3684 AAGGCGAGCCCGAGACGATGAGGCGGAGGAGAAAGCGCGACGCCACGAAGGAGGATTTA 3743  
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QY 3744 GGTCTCGACGAGGAACCTGACGAGGAGGCGGAATCGAGAGGCGCCGCTCGACGGTGAT 3803  
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QY 3804 ATCATTTATTCATGCACACGACGAGGATATCTCGATGAATATCCAGCTGATTGCTGCCCC 3863  
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QY 3924 GGATGGGGCAATTTACGACTGAAACATTTTCGATTATGAGGATAAATTTTGAACA 3983  
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QY 4104 TTCCTCTGGAAATGTTAAATCAAGTGTGTGGCGTCGGCTTCAAGTGTACTTGACCAAC 4163  
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QY 4164 CGGTGTGTGGCTCGATTTGCTGATTTGCTATGCTATGCTTATCAACTTCGTTGCTTCA 4223  
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QY 4224 CTTGTTGGAGCTGGTGTATTCAGCCCTTCAAGACTATGCGAAGCTTTAAGACACTGAGA 4283  
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QY 4284 CCAGTACGTGCCATGTCGGTATGCGAGGATAGAGGTGCTGCTTAATGGCTGGTACAA 4343  
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QY 4824 TATAGTGCATGATGAAAGATGGGCTCTAAAAAACCAATTAAGGCCATTCGAACCAAGG 4883  
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Db 601 GGTTCATTATTTACCGGTTTACGTATCTTAGAGATCATGGGAATGGCTGGACTTCGTA 660  
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QY |||||  
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Db 2638 GGTTCCAGGGCTGTGCCGTATTTGCGGTTCTTCGATTTGCTGCGTGTATTTCAAACTGGCC 2697

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QY 5064 TGCTATTAATAATATTCGCTTTACGATATCAGTATTTTATTTGAGCCATGGAATTTATTT 5123  
|||||











QY	5409	GAGCTTCAACA	TTCAAGACCTTTGGCCAGACGATGATCCCTGCTCTCTTCAGATGTCGACG	5468
Db	5365	TCAGCCGGTTGGGATGGTGTGTAGATGCCATTTATCAATGAGGAAGATTTGGGATCCACCC	5424	
QY	5469	TCAGCCGGTTGGGATGGTGTACTGCGACGCCATTATCAATGAGGAAGCATGCGATCCACCC	5528	
Db	5425	GACAACGACAAGGCTATCCCGGGCAATTTGGTTCAGCGCATGTTGGAATTAACGTTTCTC	5484	
QY	5529	GACAGCGACAAAGGCTATCCGGGGCAATTTGGTTCAGCGACCGTTGGAATAACGTTTCTC	5588	
Db	5485	CTTTCATATCTAGTTATAGCTTTTGTAGCTTTATTAATATGTCATCTGCTGTCATCTC	5544	
QY	5589	CTCTCATACCTAGTTATAGCTTTTGTAGCTTTATTAATATGTCATCTGCTGTCATCTC	5648	
Db	5545	GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGCTCTCACCGCAGCAGGATTACGAT	5604	
QY	5649	GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTTAACCGCAGGACTAGAC	5708	
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCGGAGGCAACCCAGTACATACGCTAGCAC	5664	
QY	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGGCACCCAGTACATACGCTATGAT	5768	
Db	5665	CAGCTGCCAGCTTCTTGACGCTGCTGGAGCCGCGCTGCAGATCCACAGCCGCAACG	5724	
QY	5769	CAGCTGTCCGAATTCCTGGACGCTACTGGAGCCCGCGCTGCAGATCCACAAACCGAACG	5828	
Db	5725	TACAAAATCATATCGATGGACATGCGGATATGTCGGGCGCACATGATCTACTGTGTGGAT	5784	
QY	5829	TACAAGATCATATCGATGGACATACCCATCTGTCGGGTGACCTCATGTACTGCTGCAC	5888	
Db	5785	ATATTCGATGCCCTGACCAAGGACTTCTTTGGCGCAAGGTTAATCCGATCGAGGAGACG	5844	
QY	5889	ATCCTCGACGCCCTTACGAAAGACTTCTTTGGCGGAAAGGCAATCCGATAGAGGAGACG	5948	
Db	5845	GGTGAATTTGGTAGATACGCGCGCGACCGGACACCGAGGGCTATGATCCGGTGTCTCA	5904	
QY	5949	GGTAGAATTTGGTAGATACGCGCGCGCGGATACGAGGGCTACGAGCCGCTCTCATCA	6008	
Db	5905	ACACTGTGGCGCAGCGTTCAGGAGTACTGCGGCAAGCTGATACAGAATTCGCTGGCG	5960	
QY	6009	ACGCTGTGGCGTCAAGCTGAGGAGTACTGCGCCCGCTTAATCCAGCACGCTGGCG	6064	
RESULT	6			
ID	US-08-808-793-1	STANDARD; DNA; UNC; 6318 BP.		
AC	XXXXXX			
DE	Sequence 1, Application US/08808793			
DT	Sequence 1, Application US/08808793			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Soderlund, David M.			
CC	APPLICANT: Ingles, Patricia J.			
CC	TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS			
CC	TITLE OF INVENTION: AND USE THEREOF			
CC	NUMBER OF SEQUENCES: 32			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Nixon, Haigraive, Devans & Doyle LLP			
CC	STREET: Clinton Square, P.O. Box 1051			
CC	CITY: Rochester			
CC	STATE: New York			
CC	COUNTRY: USA			
CC	ZIP: 14603			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/808,793			
CC	FILING DATE:			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			

Qy	867	CTGTCGGTGTTCCGCGTTGATGGCGCTACAGATCATATATGCGCGCTGCTCACCGAGAAAGTGC	926
Db	871	ATTAAACGATATCCCCTGGACGGCAGATTGGGGCAATCTGACCGATGAAAACCTGTTTCTA	930
Qy	927	ATCAAGAGTTCCCGCTGGACGGTTCCTGGGCAATCTGACCGACGAGAACCTGGGACTAT	986
Db	931	CACAATAGACAAGTTCCAAATTTGGTTTACGAGAGAACCATGGCAGTTCATATCCGGTGTGC	990
Qy	987	CACAATCGCAATAGCTCCAAATTTGGTATTTCCGAGGACGAGGGCATCTCATTTCCGTATATGC	1046
Db	991	GGGAATGATATCCGGTGGGAGCAATTCGGCGCAGGATTACGTCCTGCTGACGAGGCTTCGGC	1050
Qy	1047	GGCAATATATCCGGTCGGGGCAATTCGACGACGATTACGTTGTGCTGCAGGGTTGGT	1106
Db	1051	CCCAATCCCAACTACGACTACACAGTTTCGATTTCATTCGGTTGGGCTTTCTCTGTCCGGG	1110
Qy	1107	CCGAATCCGAATATATGGCTACACCAAGCTTCGATTTCGTTTCGGATGGGCTTTCTGTCCCGC	1166
Db	1111	TTTCGTCATGATACCCAAGATTTCCTGGGAGGATCTGATACGACGTTGCTGCAAGCAGCT	1170
Qy	1167	TTCCGGCTGATGACACAGGACTTCCTGGAGGATCTGTACCAAGTCTGTTGTGTGCGCGCGGC	1226
Db	1171	GGACCTCGGCACATGTTGTTCTTTATAGTCATCATCTTCTCTAGGTTCAATTCTATCTTTGG	1230
Qy	1227	GGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCTCTAGGTTCAATTCTATCTTTGG	1286
Db	1231	AATTTGATTTGGCCATGTTGCCATGCTTTATACGAATTTGCAAAAGAAAGGCCGAAGAA	1290
Qy	1287	AATTTGATTTGGCCATGTTGCCATGCTGTATGACGAATTTCAAGAGAACGCCGAAGAA	1346
Db	1291	GAAGAGGCTGCCGAGGAGGAGCGATACGAGAAAGCTGAAGAACGGCGAGCAAGGCG	1350
Qy	1347	GAAGAGGCTGCCGAGGAGGAGCGATACGTAAGCGGAAGAAGCTGCCGCGGCCAAAGCG	1406
Db	1351	GCCAACTGGAGAGCGGGCCAAATGTAGCAGCTCAAGCGGCTCAGGATGCAGCGGATGCC	1410
Qy	1407	GCCAACTGGAGAGCGGGCCAAATGGCAGGCTCAGGAGCAGCGGATGGGCTGCCGCGC	1466
Db	1411	GCTCGGCAGCTCTGCATCCGAGATGGCAAAAGAGTCCACGCTACTCTTGCAATTAGCTAT	1470
Qy	1467	GAAGAGGCTGCATCGTCATCCGAAATGGCCAAAGTCCGAGCTTCTTGCATCAGCTAT	1526
Db	1471	GAATGTTGTTGGCGGAGAGGCAACGATGACACAAACAAGAGAGAGATGTCCATA	1530
Qy	1527	GAGCTATTTGTTGGCGGAGAGAGGCAACGATGACAAACAAGAGAGAGATGTCCATT	1586
Db	1531	CGCAGCTCGAAGTGAATCGGAGTCCGTTATACAAAGACAACACGACCTTACC	1590
Qy	1587	CGGAGCGTCTGAGTGTGAGTCTGGAGTCTGGTATACAAAGACACACGACCTTACC	1646
Db	1591	ACAGCAC--CC--GCTACTAAAGTCCGTAAGTTAGCAGACGTTCTGTTTACCTTGGT	1647
Qy	1647	ACAGCACACCAAGCTACCAAGTTCGTAAGTGGACACACATCCCTTACCTTACCTTGGT	1706
Db	1648	TCACCATTTACCTTACCGCGGGATCAGTTACACAGGTACACAAATACGAAATGGG	1707
Qy	1707	TACCGTTTAACTACGCGAGGGATCAGTATGTTCTCACAGTACACGATACGAGACGA	1766
Db	1708	CGTGACGCTTTTGGTATACCAAGTACGATTCGCAAGCCATTGGTACTGCAACATATCAG	1767
Qy	1767	CGTGCGCGTTTGGTATACCGGTAGCGATCTGTAAGCCATTGGTATGTTCAACATATCAG	1826
Db	1768	GATGCCGACGACGATTTGCCCTATGCCGATGACTCGAATGCCGTAAACCAATGTCCGAA	1827
Qy	1827	GATGCCGACGACGACTTGCCTATTCGCCGAGGATCGAATGCCGTACCCCCGATGTCCGAA	1886
Db	1828	GAGAATGGTGCAATTATAGTACCAGCCTACTATTGTAATTTAGTTTCTAGACATTTCTCA	1887
Qy	1887	GAGAATGGGGCCATCATAGTCCCGTGTACTATGGCAATCTAGGCTCCCGACACTCATCG	1946
Db	1888	TATACCTCGCATCAATCAAGAATCTCTGTATACATCATCATGGTGTGATTTATTTGGTGGCATG	1947
Qy	1947	TATACCTCGCATCAGTCCGGAATCTGTACTCTACATGGGATCTACTTGGCGGCAATG	2006

1948	Db	GGCGCCATCGGTCGCCAGCACAATGACCAAGAGAGACAAATGGCGAGTCGCCACACACGC	2001
2007	Qy		2066
	Qy	GGCGTATCGGGCGTCAGCAATGATGACCAAGAGAGACAAATGGCGAACCCGACACACACGC	
2008	Db		2067
	Qy	AATCAATCAATCGGTCTGTCACACCAATCGTGGCAGTAGTAGCGGCTGGTGGCTATGCC	
2067	Qy		2114
	Qy	AATCAATCAAGT-GG-GC-GCCACCAGTGGCGCACCA---C-CTG-TC-TGGACA--CC	
2068	Db	GATGCCAATCACAAAGGAACAAAGGATTATGAATGGGTGAGGATTATACAGACGAAAGCT	2127
	Qy		2171
2115	Qy	AATCACAGCTC---GATCATCGGACTACGAAATGGCCCTGGAGTGCACGGACGAAAGCT	
	Db		2187
2128	Db	GGCAAAATAAACACACACACAGACAATCCTTTTATCGAGCCCGTCCCAAACCTCAACAGATGGTA	2187
	Qy	GGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACACAAACGGTGGTT	2231
2188	Db	GACATGAAGATCTTATGTGCTTAAATGATATCAATGAACAAGCGGTGGTGGCGCATAGT	2247
	Qy		2291
2232	Qy	GATATGAAGATGATGATGCTGCTGATGACATCATCGAACAGGCGGTGGTGGCGACAGT	
	Db		2283
2248	Db	CGTGCTAGTGAACAGAGTG-----AGGACGATGACGAAGAT	2283
	Qy	CGGCAAGCGATCGCGGTGCTCCGCTTACTATTTCCTCCACAGAGGACGATGACGAGGAT	2351
2284	Db	GGTCCCACTTCAAGGACATCGCCCTCGGAATACATCTTAAAGGACATCGAAATCTTTTGT	2343
	Qy	GGCGGACGTTCAACACACAGGCACTCGAAGTGATCCTCAAGGACATCGATGTTTGT	2411
2344	Db	GTATGGGACTGTTGTTGGGTGGTTTAAAAATTCAGGAATGGGTGCTCTTTATTGTGTTTC	2403
	Qy	GTGTGGGACTGTTGCTGGGTTTGTTTGAATTTTCAGGAGTGGGTATCGCTCATCGCTTTC	2471
2404	Db	GATCCATCTGGAGCTCTTCATACCCCTGCTATTGTGTGTCAAATACGATGTTTATGGCC	2463
	Qy	GATCCCTCTGTCGAGCTCTTCATCAGCTGTGCAATGGTCAACACGATGTTCAATGGCA	2531
2464	Db	ATGGATCATCACACATGAATCCGGAATTAGAGAAGTGCTGANAAGTGGTAACATTTTC	2523
	Qy	ATGGATCACCACGATATGAACAAGGAGATGGAACGCGTCTCAAGAGTGGCAACTATTTC	2591
2524	Db	TTACGGGCACTTTTGCAATTTGAAGCCAGCATGAACACTGATGCCATGAGCCGGAAGTAC	2583
	Qy	TTACCGGCACTTTGGCATCTGAGGCCCACCATGAAGCTAATGCCATGAGCCCCAAGTAC	2651
2584	Db	TACTTCCAGGAAGCTCGGAACATTTTCGATTTTCATATTGTGGCCCTGTCTCTGCTGGAA	2643
	Qy	TATTTCCAGGAGGCTCGGAACATCTCGACTTCATTTATCGTGCCCTATCGCTATTGAA	2711
2644	Db	TTGGGCTTGGAGGTGTCAGGGCCCTGTCGGGTGTGAGAAGTTTTGCTTGTCTGCTGTA	2703
	Qy	CTGGGACTCGAGGGTGTCCAGGGTCTCTCCGTATTCCGTTCTCTTCGATTTGCTGGTGTGTA	2771
2704	Db	TTCAATTTGGCAAAATCATGSCCCACACTCAATTTACTCATTTTCGATTTAGGCCGGAACA	2766
	Qy	TTCAACTGGCCAACTCTTGGCCCCACACTTAATTTACTCATTTTCGATTTAGGACGACC	2831
2764	Db	ATGGGTGCATTTGGTAACTCTGACATTTGTACTTTTGCATATCACTTCATCTTGGCGTG	2822
	Qy	ATGGGCGCTTTTGGGTAACTCTGACATTTGTACTTTTGCATATCACTTCATCTTTCGCGTG	2891
2824	Db	ATGGGAATGCAACTTTTCGGGAAGAACTATATTGACCACAAAGGATCGCTTCAAGGACCAT	2881
	Qy	ATGGGAATGCAACTTTTCGGGAAGAACTATTCATGATCACAAAGGCCCTTTCCGGATGCG	2951
2884	Db	GAATTAACCGCGTGGAACTTCCAGCGACTTCATGCACAGCTTTCATGATTTGTTTCGAGTG	2941
	Qy	GACCTGCCGCGCTGSAACTTCCACGACTTTATGCACAGCTTTCATGATCTGTTTCCGGGTG	3011
2944	Db	CTGTGGGAGATGGATCGATCGATCTCATCTGGAGCTGCGATGTTATGTCGGCGCATGTCACTGT	3001
	Qy	CTCTCGGGAATGATGATCGATCGATCTCATCTGGAGCTGCGATGTTATGTCGGCGCATGTCTGCTG	3071





Db 751 GGTCTGTCTAATGTAATCTGTAATAAATCTACGGCATGTGATATTTTGCAAAATGTTTTC 810  
QY 807 GGCCTGTCTAATCGGTGAAGAAATCTCGCGATGTGATTAATCTGACCAATGTTCTCC 866  
Db 811 CTGTCGGTGTTCGGCTGATGGGCTTACAATCTATATGGGTGTTCTTAACACAAAAGTGC 870  
QY 867 CTGTCGGTGTTCGGCTGATGGGCTTACAGATCTATATGGGCGTGTCTACCGAGAAGTGC 926  
Db 871 ATTAACGATTCCTCCCTGGAGCGGAGTGTGGGCAATCTGACCGATGAATGTTTCTTA 930  
QY 927 ATCAAGAAGTTCCTCGCTGGAGCTTCCTGGGCAATCTGACCGAGAGAATCTGGGACTAT 986  
Db 931 CACAATAGCAACAGTTCCTAATGTTTACGAGAGAACCATGCGGAGTCTATATCGGTGTGC 990  
QY 987 CACAATCGCAATAGCTCCAAATGTTTACGAGAGAACCATGCGGAGTCTATATCGGTGTGC 1046  
Db 991 GGGAAATGATCCGGTGGGACAAATGCGGCAAGATTACGCTCTGCTGCAAGGGCTTCGGC 1050  
QY 1047 GGCATATATCCGGTGGGCAATGCGAGCAGATTACGTTGCTGCAAGGGTGTGGT 1106  
Db 1051 CCGAATCCCAACTAGACTACACAGATTTCGACTCATATCGGTGGGCTTTCCTGTGCGGG 1110  
QY 1107 CCGAATCCGAATATAGCTACACAGCTTCGATTCTGTTGCGATGGGCTTTCCTGTGCGGC 1166  
Db 1111 TTTCTCTCATGACCCCAAGATTTCTGGAGAGTCTGTATCAGCAGCTGCTGCAAGCAGCT 1170  
QY 1167 TTCGGCTGATGACACAGACTTCTGGAGAGTCTGTACCACTGGTGTGCGGCGCGCC 1226  
Db 1171 GGACCTGGCACATGTTGTTCTTTATAGTATCATCTCTCTAGGTTTCATTTCTATCTTGTG 1230  
QY 1227 GGACATGGCACATGCTGTTCTTTATAGTATCATCTCTCTAGGTTTCATTTCTATCTTGTG 1286  
Db 1231 AATTGATTTTGGCCATGTTGCCATGTCCTTATGACGAATGCAAAAGAGCGCGAAGAA 1290  
QY 1287 AATTGATTTTGGCCATGTTGCCATGTCGTATGACGAATGCAAAAGAGCGCGAAGAA 1346  
Db 1291 GAAGAGCTCCGAGGAGGAGCCATCCGAGAAGCTGAAGAGCGGAGCAGCAAGCGG 1350  
QY 1347 GAAGAGCTCCGAGGAGGAGGAGGATACGTGAAGCGGAAGCTGCGCGCGCCAAAGCG 1406  
Db 1351 GCCAACTGGAGAGCGGGCAATGTAGCAGCTCAAGCGGCTCAGGATGACAGCGGATGCC 1410  
QY 1407 GCCAAGCTGGAGAGCGGGCAATGCCAGGCTCAGGAGCAGCGGATGCGGCTGCGGCC 1466  
Db 1411 GCTCGGGAGCTCTGCATCCCGAGATGGCAAAGAGTCCGAGTACTCTTGCAATTAGTAT 1470  
QY 1467 GAAGAGGCTGCACCTGCATCCGGAATGGCCAAAGTCCGAGCTTCTTGCAATCAGCTAT 1526  
Db 1471 GAACGTGTTTGGCGGAGAGGGCAACGATGACACACACAGAGAGAGATGTCGATA 1530  
QY 1527 GAGCTATTTTGGCGGCGAGAGGGCAACGATGACACACACAGAGAGATGTCGATT 1586  
Db 1531 CGCAGCTCGAAGTGGAACTCGGAGTCCGAGCTGAGCGCTTATACAAAGACACACACCTACC 1590  
QY 1587 CGGAGCTCGAGGTGGAGTCCGAGTCCGAGCTGAGCGCTTATACAAAGACACACACCTACC 1646  
Db 1591 ACAGCAC-CC--GGTACTAAAGTCCGTAAGATTAGCAGACTTCCCTATCCTTACCTGGT 1647  
QY 1647 ACAGCACACCAAGCTACCAAGTTCGTAAGTGAAGCAGCAGATCCTTATCCTTACCTGGT 1706  
Db 1648 TCACCATTTTAACTACGCGCGGGATCAGTAGTTTCACACAGTACACAAATACGAATGGG 1707  
QY 1707 TCACCGTTTAACTACACAGGGGATCAGTAGTTTCTCACAAGTACACGATACGGAACGGA 1766  
Db 1708 CGTGAGCTTTTGTATACCAAGTAGCGATCGCAAGCATCTGGTACTGCAACATATACAG 1767  
QY 1767 CGTGCGCTTTTGTATACCGCGTAGCGATCGTAAGCCATTGGTATGTTCAACATATACAG 1826  
Db 1768 GATGCCAGCAGCACTTTGCCCTATGCCGATGACTCGAATGCCGTAAACCACTATGTCGGAA 1827  
QY 1827 GATGCCAGCAGCACTTTGCCCTATGCCGATGACTCGAATGCCGTAAACCACTATGTCGGAA 1886  
Db 1828 GAGAATGTGCGCATATATAGTACCAGCCTACTATTGTAAATTTAGGTTCTTAGACATCTTCA 1887

QY 1887 GAGAAATGGGCCATCATAGTCCCGTGTACTATGGCAATCTAGGCTCCCGACACTATCG 1946  
Db 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCATCATGGTGAATTTATTTGGGTGGCATG 1947  
QY 1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTCATATGGCATCTACTCGGGCGCATG 2006  
Db 1948 GCGGCCATGGGTCCAGCACAATGACCAAGAGAGCAAAATGGCCAGTCCGACACACAGC 2007  
QY 2007 GCGCTCATGGGCTCAGCACAATGACCAAGAGAGCAAAATGGCCAGTCCGACACACAGC 2066  
Db 2008 AATCAATCAATCGGTGCTCAACCAATGGTGGCAGTAGTACGGCCGGTGGGTGCTATCCC 2067  
QY 2067 AATCAATCAAT-GG-GC-GCCACCAATGGCGGCACAC--CTGTC--TGA--C-A--CC 2114  
Db 2068 GATGCCAATCACAAAGAACAAAGGATTAATGAATGGGTCAAGATTATACAGACGAAGCT 2127  
QY 2115 AATCACAAAGTCT--GATCATCGGACTACGAATTTGGCTGGAGTGCACGGACGAAGCT 2171  
Db 2128 GGCAAAATAAACCACACGACACATCTTTTATCGAGCCGCTCCAAACTCAACAGTGGTA 2187  
QY 2172 GGCAGATTAAACATCATGACAAATCTTTTATCGAGCCGCTCCAGACACAAACGGTGGT 2231  
Db 2188 GACATGAAGATGTTATGGTCTTAAATGATATCAATGAACAAGCGCTGTCGGCATAGT 2247  
QY 2232 GATATGAAGATGTTATGGTCTTGAATGACATCATCGAACAGCGCGTGGTGGCAGAGT 2291  
Db 2248 CGTGCTAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283  
QY 2292 CGGCAAGCATCGCGGTGCTCCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351  
Db 2284 GGTCCCACTTCAAGACATCGCCCTCGAATATATCTTAAAGGCATCGAAATCTTTTGT 2343  
QY 2352 GGGCCGAGTTTCAAGACAAAGGCACTCGAAGTATCTTCAAGGSCATCGATGTGTGT 2411  
Db 2344 GTATGGACATGTTGGGTGTTGTTAAATTTCAAGAAATGAGGCTCTCTTATTTGCTTC 2403  
QY 2412 GTTGGACATGTTGTTGGTGTGTTGAAATTTCAAGAGTGGGTATCGCTCATCGCTTC 2471  
Db 2404 GATCCATTCGTGAGCTCTTCAATACCTGTATTTGGTGTCAATACAATGTTTCATGGCC 2463  
QY 2472 GATCCCTTCGTGAGCTCTTCAACACGCTGTCATCTGTCGTCGTCGTCATGTCGCA 2531  
Db 2464 ATGATCATCACACATGAATCCGGAATTCGGAGAGTGTGTAAGTGTGAATCTTTC 2523  
QY 2532 ATGATCATCACACATGAATGAACAGAGATGGAACGCGTCTCAAGAGTGCACATTTTC 2591  
Db 2524 TTCAGGCCACTTTTGAATTTGAGGCCAGCATGAAACTGATGGCCATGAGCCGAGCTAC 2583  
QY 2592 TTCAGGCCACTTTTGGCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCGAGCTAC 2651  
Db 2584 TACTTCCAGGAAGCTGGAAACATTTTCGATTTCATTTATTTGGCTTGTCTCTCTCGAA 2643  
QY 2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTTATCTGTCGCTTCATCTGTCGAA 2711  
Db 2644 TTGGCCTCGAGGCTGTCAGAGGCTGTCGGTGTGAGAAAGTTCCTTTCGTCGTCGTA 2703  
QY 2712 CTGGACTCGAGGCTGTCAGGCTGTCGGTATTTGCGTCTCTTCGATTTGCTGCTGTA 2771  
Db 2704 TTCAAATTCGAAATCATGCCCCACACTGAATTTACTCATTTTCGATTTATGGCCGAGCA 2763  
QY 2772 TTCAACTGCCAAGTCTTGCCCCACACTTAATTTACTCATTTTCGATTTATGGACGACC 2831  
Db 2764 ATGGGTGCATTTGGTAACTCTGACATTTGACTTTGCAATTTATCTTCTTTCGCTG 2823  
QY 2832 ATGGCGCTTTGGTAACTCTGACATTTGACTTTGCAATTTATCTTCTTTCGCTG 2891  
Db 2824 ATGGAAATCAACTTTTCGAAAGAACTATATTGACCAAGGATCGCTTCAAGACCAT 2883  
QY 2892 ATGGAAATCAACTTTTCGAAAGAACTATATCATGATCAACAGGACCGCTTTCGAGTGC 2951  
Db 2884 GAATTACCGCTGGAAATTTTACCGGACTTTCATGACAGACTTTCATGATTTGTTCCGAGT 2943



QY 2952 GACCTGCCGCTGGAACCTTCAACGACTTTATGACACAGCTTCATGATCGTGTTCGCCGGTG 3011  
Db 2944 CTGTGCGGAGTGGATCGAGTCATCTGGGACTCTGCATGTATGTGGCGGATGTCAGCTGT 3003  
QY 3012 CTCTGCGGAGAAATGGATCGAGTCATCTGGGACTCGCATGTACGTGGCGGATGTCGTGC 3071  
Db 3004 ATACCCCTCTCTTGGCCACCGGTGCTGATCGGCAATTTTGTGTCTTAACTTTTCTTA 3063  
QY 3072 ATTCCCTCTCTTGGCCACCGGTGCTGATCGGCAATCTTGTGTACTTAACTTTTCTTA 3131  
Db 3064 GCTTTGCTTTTGTCCAACTTCTGGTTCATCTAGTTTATCAGCCCGGACTCCGCAATGAT 3123  
QY 3132 GCCTTGTCTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGGACTCGCGATAAGAT 3191  
Db 3124 ACCAATAAATAGCAGAGCGCTTCAATCGTATTCTCGTTTAAAGAACTGGGTGAACAGT 3183  
QY 3192 ACGAATAAATAGCGAGCGCTTCAATCGAATGGCCGATTTAAAGATTGGGTTAAGCGT 3251  
Db 3184 AATATTGCCGATTTGTTTAACTTAATTCGAAATAAATGCAAAATCAATAAGTGACCAA 3243  
QY 3252 AATATTGCTGATTTTCAAGTTAATAGTTAACAATTTGACAAATCAATAAAGTGATCAA 3311  
Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265  
QY 3312 CCATCAGGTGAGAGACCAACGATCAGTTAGTTTGGAGCGAGAGCATGGTGACAAC 3371  
Db 3266 -AACTGGAGTTGGGTCAATGCAAAATCATGGCGATGGCTTGATCAAAAAGGGTATGAAG 3324  
QY 3372 GAACTTGGAGCTGGGCCACGACGAGATCTCGCCGACGGCTCATCAAGAAGGGATCAAG 3431  
Db 3325 GCGCAGCCAGCTGGAGGTGGCCATTTGGCGATGGCATGGAGTTTCACGATACATGGGGAT 3384  
QY 3432 GAGCAGACCAACTGGAGTGGCCATCGGGATCGGATCGGAATTCACGATACACGGCGAC 3491  
Db 3385 ATGAATAACACAGCCCAAGAAATCAAAATTCATAAACAACACACGATGATTGGAAAC 3444  
QY 3492 ATGAAGAACAACGCCGAAGAAATCCAAATATCTAAATACGCANCCGATGATTGGCAAC 3551  
Db 3445 TCAATAAACACCAAGACAATAAGACTGGAACATGAGCTAAACCATAGAGTTTGTCCATA 3504  
QY 3552 TCAATTAACCAACAGACAATAAGACTGGAACACGAGCTAAACCATAGAGTTTGTCCATA 3611  
Db 3505 CAGGAGATGACATGCCAGCATTAATCTCATATGTAGTACCCATAAAGATCGACCATCAAG 3564  
QY 3612 CAGGACGACGACTGCCAGCATTAATCTCATATGTAGTACCCATAAAGATCGACCATCAAG 3671  
Db 3565 GACGAGAGCCACAAGGCGACGCGAGACCATCTGAGGGGAGGAGAAACCGCACGTCACG 3624  
QY 3672 GACGAGAGCCACAAGGCGACGCGAGACCATCTGAGGGGAGGAGAAACCGCACGCGCAGC 3731  
Db 3625 AAAGAGGACCTCGGCCCTCGACGAGGAACCTGGACGAGGAGCGCGAGGGGATGAGGGCCAG 3684  
QY 3732 AAGGAGATTAGTCTCGACGAGGAACCTGGACGAGGAGCGCGAATTCGCGAGGGGCGCG 3791  
Db 3685 CTGGATGGTGCATCATATTCATTCATGCCCCAAACGACGACGAGATATCGACGACATCCG 3744  
QY 3792 CTCGAGGGTGATATCATATTATCATGACA---CGACGAGGATATCTCGATGAATATCCA 3848  
Db 3745 GCGGACTGTTTCCCGGACTCTGACTACAAGAGTTTCCGATCTTGGCCGCGCGACGAGGAC 3804  
QY 3849 GCTGATTTGCTGCCCGGATTCGTAATATGAGAAATTTCCGATCTTACGCGGTGACGATGAC 3908  
Db 3805 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTAATTTGAAAT 3864  
QY 3909 TCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAACCTTTTCAATTAATTTGAAAT 3968  
Db 3865 AAATATTTGAACCCGAGTTATCACTATCATTTTAAATGAGTGTAGCTTTGGGCTTA 3924  
QY 3969 AAATATTTGAACAGCTGTTATCACTATCATTTTAAATGAGTGTAGCTTTGGCATTA 4028  
Db 3925 GAAGATGTTTATACCCGATCGACCTGTGATCGAGGATATCTGTACATGAGGACG 3984  
QY 4029 GAAGATGTACATCTGCCACAAGACCCCATCTGCAGGATATTTTATACATATATGGACAGA 4088

Db 3985 APATTTACGGTGATATCTTTTGGAGATGTTGATCAAAATGGTTGGCCCTGGGCTTTAAG 4044  
QY 4089 APATTTACGGTTATATCTTCTTGGAATGTTAAATCAAGTGGTTGGCGCTCGGCTTCAA 4148  
Db 4045 GTCTACTTACCAATGCTGTTGGCTGGATTTGCTGATTTGCTGATCTATCGCTTATA 4104  
QY 4149 GTGTAATTTACCAACCGTGGTGGCTGATTTGCTGATTTGCTGATGATGATCGCTTATC 4208  
Db 4105 AATTTGGTTTGGCTTGGTTCGGGCTTAAATGATATPAGCGGTTTATAGATCAATGGCACA 4164  
QY 4209 AACTTCGTGCTTCACTTGTGGAGCTGGTGTATCAAGCGCTTCAAGACTATGCGAACG 4268  
Db 4165 CTGCGGCGCCTTAAGCCATGCGTCTGTCTAGATGGGAGGGTATGAAAGTTGTCGTG 4224  
QY 4269 TTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGCGATGAGGCTCGCTT 4328  
Db 4225 AATGCGCTGTTCAAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTCTGATATTT 4284  
QY 4329 AATGCGCTGTTCAAGCTATACCGTCCATCTTCAATGTCTATTTGGTGTCTGATATTT 4388  
Db 4285 TGCTTATTTTGGCATTATGGAGTACAGCTTTTGGCTGGAAATATTTTAAAGTGTAAA 4344  
QY 4389 TGGCTAATTTTGGCATAATGGTGTACAGCTTTTGGCTGGAAATATTTTAAAGTGGCAG 4448  
Db 4345 GATGGTAATGACACTGTGCTGAGCCATGAATCATACCGAATCGTAATGCCCTGCAAAAGT 4404  
QY 4449 GACATGAATGGCAGAGCTCAGCCACGAGATCATACCAATCGCAATGCCATGCCGAGAGC 4508  
Db 4405 GAAACTTACACCTGGGAAATATCGCAATGAATTCGATCATGTAGTAAATCGGTATCTC 4464  
QY 4509 GAGAATCATACGCTGGTGAATTCAGCAATGAATTCGATCATGTAGTAAACGCTATCTG 4568  
Db 4465 TGCTTATTTCAAGTGGCCACCTTTAAGGCTGGATCCAGATTAAGAACGATGCCATGAT 4524  
QY 4569 TGGCTTTTCCAGTGGCCACCTTCAAGGCTGGATCAATCATGAACGATGCTATCGAT 4628  
Db 4525 TCAGGAGGTGGACAGCAGCGGATCCGAGAACCAATATCTACATGTATTTATATTTTC 4584  
QY 4629 TCAGGAGGTGGACAGCAGCAACCAATTCGTGAACGACATCTACATGTATTTATTTTC 4688  
Db 4585 GTATTTCTCATATATTTGGATCATTTTTCACACTCAATCTGTTCATTTGGTGTATCATTT 4644  
QY 4689 GTATTTCTCATATATTTGGATCCTTTTTCACACTCAATCTGTTCATTTGGTGTATCATTT 4748  
Db 4645 GATAATTTTAAATGAACAAAGAAAGAGAGGTGGATCATTAGAAATGTTTCATGACAGAA 4704  
QY 4749 GATAATTTTAAATGAGCAAAAAGAAAGAGGTGGATCATTAGAAATGTTTCATGACAGAA 4808  
Db 4705 GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAAAAAACCATTTAAAGCC 4764  
QY 4809 GATCAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAAAAAACCATTTAAAGCC 4868  
Db 4765 ATTTCAAGACCGGAGGTGGCCACCAAGCAATAGTATTCGAAATAGTTTACAGATAAAAA 4824  
QY 4869 ATTTCAAGACCGGAGGTGGCCACCAAGCAATAGTCTTTGAAATAGTTTACCGATAAGAA 4928  
Db 4825 TTCGATATATCATATTTGTTGCTTAAACATGTTTACCATGACCCCTCGATCGG 4884  
QY 4929 TTCGATATATCATATTTGTTGCTTAAACATGTTTACCATGACCCCTCGATCGT 4988  
Db 4885 TACGACGCTCCGAGGCGTACAACATGCTCTCGACAAACTCAATGGGATATTCGTAGTT 4944  
QY 4989 TACATGGCTGGACAGTAAACGCGTCTCTAGACTATCTCAATGCGATATTCGTAGTT 5048  
Db 4945 ATTTTCAAGTGGCGAATGCTTATTAATAATATTCGCTTTAGCATATCACTATTTCAAAGAG 5004  
QY 5049 ATTTTCAAGTGGCGAATGCTTATTAATAATATTCGCTTTTACGATATCACTATTTTATTGAG 5108  
Db 5005 CCATGGAATTTTATGATGTAGTTGTCTATTTTATCCATCTTTAGCTTGTGTACTCAGC 5064  
QY 5109 CCATGGAATTTTATGATGTAGTTGTCTATTTTATCCATCTTTAGGCTGTGTACTTAGC 5168



Db	5065	GACATCATTTGAGAAGTATTTTCGTATCGCCGACACATGCTCCGTGTGGTGAGAGTGGCCAAA	5124
QY	5169	GAATATTATCGAAGAAGTACTTCGTGTCGCCGACCCCTGCTCCGAGTGGTGTGCTGTGGCGAAA	5228
Db	5125	GTGGGTGCTGTCTCTCGGTTTGTAGTCAAGGGTGCCAAGGGTATCCCGACGTTGCTGTGTCGCG	5184
QY	5229	GTGGGCGGTGTCTTTCGACTGTGTGAAGGGAGCCCAAGGGCATTCGGACACATGCTCTTCGCG	5288
Db	5185	TTAGCCATGTCGTGTCGTCGCCCTTATTCAACATTTGTCTGTTGCTTCTTTGGTGATGTTTC	5244
QY	5289	TTGGCCATGTCGTGCGCGGCCCTGTTTCAACATCTGCTCTGCTGTCTGTGTTCTCTGGTCATGTTTC	5348
Db	5245	ATCTTTGCTATCTTTTGGCATGTCCTTCTTTCATGATGTCAAAGAGAGAGCGGCATAAAT	5304
QY	5349	ATCTTTGGCATTTTCGGCATGTCGTCTTTCATGACGTGAAGGAGAAGCGGCATTAAAC	5408
Db	5305	GCTGTGTATAATTTTAAGACATTTGGCCAAAAGTAGTATTGCTGTTTCAAGATGTCCTAAC	5364
QY	5409	GACGCTCTACAACCTTCAAGACCTTTTGGCCAGAGCATGATCCTGCTCTTTCAAGATGTCGACG	5468
Db	5365	TCAGCCGCTTGGGATGGTGTGTAGATGCCATTATCAATGAGGAAGATTTGGGATCCACCC	5424
QY	5469	TCAGCCGCTTGGGATGGTGTACTGACGCCATTATCAATGAGGAAGCATGCGATCCACCC	5528
Db	5425	GACAACGACAAGGGCTATCCGGGCAATTTGTGGTTCAGGCACTGTTGGAATTTACGTTTCTC	5484
QY	5529	GACAGCGACAAAGGCTATCCGGGCAATTTGGTTCAGCGACCGTTGGATAACGTTTCTC	5588
Db	5485	CTTTCAATCTAGTTATAAGCTTTTGTGATGTTATTATAATGTAACATGCTGTGCTCATTTCTC	5544
QY	5589	CTCTCATCTAGTTATAAGCTTTTGTAGTTATTATAATGTAACATGCTGTGCTCATTTCTC	5648
Db	5545	GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGGTCTCACCGAGGAGCTATGAT	5604
QY	5649	GAGAACTATAGTCAGGCCACCGAGGAGCTGCAGAGGGTCTAACCGACGACGACTAGCAC	5708
Db	5605	ATGTACTACGAGATTGGCAACAATTCGATCCGGAGGATACCCAGTACATAAGATACGAC	5664
QY	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCGAGTCTCTGACGCTGTGAGCGCCGCTGACAGTCCACAGCCGAAACAG	5724
QY	5769	CAGCTGTCGAAATCTCTGACGCTACTGAGCGCCCGCTGACAGTCCACAAACCGAAACAG	5828
Db	5725	TACAAATCATATCGATGACATGCCGATATGTCGGGCGGACATGATGCTACTGTGTGGAT	5784
QY	5829	TACAAGATCATATCGATGGACATACCCATCTGTGCGGTGACCTCATGCTACTGGCTGAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTCTTTTGGCGGCAAGGGTAAATCCGATCGAGGAGACG	5844
QY	5889	ATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGACG	5948
Db	5845	GGTGAATTTGGTAGATTTCGCGCGCGACCGGACACCGAGGGCTATGATCGGGTGTCTGTCG	5904
QY	5949	GGTAGATTGGTAGATACAGGCCCGCCCGGATACGGAGGGCTACGAGCCCGCTCTCATCA	6008
Db	5905	ACACTGTGGCGCGAGCGTGAAGGAGTACTGCGCCAAAGCTGATACAGAATTCGGTGGCG	5960
QY	6009	ACGCTGTGGCGTTCAGCGTGAAGGACTGTGCGCCCGGCTTAATCCAGACGACGCTCGCG	6064

RESULT 8  
ID US-08-808-793-2 STANDARD; DNA; UNC; 6315 BP.  
AC xxxxxx

Sequence 2, Application US/08808793  
Sequence 2, Application US/08808793  
GENERAL INFORMATION:  
APPLICANT: Soderlund, David M.  
APPLICANT: Ingles, Patricia J.  
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
TITLE OF INVENTION: AND USE THEREOF  
NUMBER OF SEQUENCES: 32

CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC	STREET: Clinton Square, P.O. Box 1051
CC	CITY: Rochester
CC	STATE: New York
CC	COUNTRY: USA
CC	ZIP: 14603
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/808,793
CC	FILING DATE:
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 60/034,361
CC	FILING DATE: 24-DEC-1996
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 60/012,649
CC	FILING DATE: 01-MAR-1996
CC	CLASSIFICATION: 435
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Braman, Susan J.
CC	REGISTRATION NUMBER: 34,103
CC	REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 716-263-1636
CC	TELEFAX: 716-263-1600
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 6315 base pairs
CC	TYPE: nucleic acid
CC	STRANDEDNESS: single
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: CDNA
SQ	SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER.
Query Match 56.38; Score 3664; DB 21; Length 6315;	
Best Local Similarity 84.8%; Pred. No. 0.00e+00;	
Matches 4980; Conservative 0; Mismatches 812; Indels 84; Gaps	
Dn	151 ATACGATATGATCAGGAGCAGGAAGTGAAGGTCCACAGCGGGATCCCACACTTGAAACAG 210
Qy	151
Dn	207 ATCCGATATGATCAGGAGCAGGAGTGAAGGTCCACACCGGATCTACACTTGAACAG 266
Qy	207
Dn	211 GGTTGCCTATACCTGTTGCAATGCAGGCGAGCTTCCGCCGGAATTGGCCTCCACTCCT 270
Qy	211
Dn	267 GGTGTGCAATACCTGTTTCGATTCGAGGCGAGCTTCCGCCGGAATTGGCCTCCACTCCT 326
Qy	267
Dn	271 CTCGAGATATCGATCCCTTCTACAGTAATGTACTGCATTTCTAGTAATAAGTAAAGA 330
Qy	271
Dn	327 CTCGAGATATCGATCCCTTCTACAGTAATGTACTGCATTTCTAGTAATAAGTAAAGA 386
Qy	327
Dn	331 AAGGATATTTTTCGTTTTCTGCTCAAAGCAATGTGGCTGCTCGATCCATTCAATCCG 390
Qy	331
Dn	387 AAAGATATTTTCGTTTTCTGATCAAAAGCAATGTGGATGCTCATTCATTCATTCG 446
Qy	387
Dn	391 ATACGTCGTAGCCATTTATATTTTAGTCATCCCTTTGTTTCGTTATTCATTATCAC 450
Qy	391
Dn	447 ATACGTCGTGGCCATTTACATTTCTAGTCATCCATTTATTTCCCTATTTCATCATCAC 506
Qy	447
Dn	451 ACTATTCTAATAATTTGATTTTAATGATAATGCCGACACAGCCCGGTGCAATCCACA 510
Qy	451
Dn	507 ACAATTCGTCAACTCGATCCCTGATGATAATCCGCAACCGCCCGTGTGAGTCCACT 566
Qy	507
Dn	511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTAGGCACGAGT 570
Qy	511
Dn	567 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGTAGGCACGAGT 626
Qy	567
Dn	571 TTCAATTTATGCCGGTTTAGCTATCTTAGAGATGCATGGAATTTGGGTGGACTTCGTAGTA 630
Qy	571

Query Match 56.3%; Score 3664; DB 21; Length 6315;  
Best Local Similarity 84.8%; Pred. No. 0.00e+00;  
Matches 4980; Conservative 0; Mismatches 812; Indels 84;

Db	151	ATACGATATGATGACGAGGACGAAGATGAAGTCCACAGCCGGATCCACACTTGAACAG	210
Qy	207	ATCCGATATGATGACGAGGACGAGGATGAAGTCCACACCCGGATCCTACACTTGAACAG	266
Db	211	GGTGTGCTTATACCTGTTTCGAAATGCAGGCGAGCTTCCGCCGGAAATGGCCCTCCACTCCT	270
Qy	267	GGTGTGCCATACCTGTTTCGATTCGAGGCGAGCTTCCGCCGGAAATGGCCCTCCACTCCT	326
Db	271	CTCGAGGATATCGATCCCTTCCTACAGTAATGTACTGACATTTCTAGTATAAGATAAAGGA	330
Qy	327	CTCGAGGATATCGATCCCTTACTACAGCAATGTACTGACATTCGTAGTTGTAAGCAAAAGGA	386
Db	331	AAGGATATTTTCGTTTTCTGGCTCAAAAGCAATGTGGCTGCTCATCCATTCAATCCG	390
Qy	387	AAAGATATTTTCGTTTTCTGCAATCAAAAGCAATGTGGATGCTCGATCCATTCAATCCG	446
Db	391	ATACGTCGTGTAGGCATTTATATTTTAGTCGATCCCTTGTTTTCGTTTATTCATTATCACC	450
Qy	447	ATACGTCGTGTGGCCATTTACATTTCTAGTCATCCCATATTTTCCCTATTTCATCATCACC	506
Db	451	ACTATTCTAACTAATGTATTTTAAATGATATGCGACAACGCCACGCCGTCGAATCCACA	510
Qy	507	ACAATTCGTCACTGCATCCCTGATGATTAATGCCGACAACGCCACGGTTGAGTCCACT	566
Db	511	GAGGTGATATTACCCGGAATCTACACATTTTGAATCAGCTGTTAAAGTATGGCACGAGGT	570
Qy	567	GAGGTGATATTACCCGGAATCTACACATTTTGAATCAGCTGTTAAAGTATGGCACGAGGT	626
Db	571	TTCAATTTATGCCGTTTACGTATCTTTAGAGATGCATGGAATTTGGGTGGCACTTCGTAGTA	630

|||||  
QY 627 TTCAATTTTGGCCGTTTACGTATCTAGAGATGTCATGGAATTTGGCTGGACTTCGTAGTA 686  
Db 631 ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGGTAAATCTCGGAGCTTTTGAAACA 690  
QY 687 ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGGTAAATCTAGCAGCCCTCGAAGC 746  
Db 691 TTTAGGCTACTGCGAGCTCTGAAACCGTAGCCATTTGTCAGGCTTAAACCAATCTGTC 750  
QY 747 TTTAGGCTGCTGCGAGGCTTTAAACCGTAGCCATTTGTCAGGCTTGAAGACCATCTGTC 806  
Db 751 GGTGCTGTCATTTGAATCTGTAAAAAATCTACGCGATGTGATAATTTTGACAATTTTTC 810  
QY 807 GGCCTGTCATCGAATCGGTGAAGAATCTGCGCATGTGATTAATCTCTGACCATGTTCTCC 866  
Db 811 CTGTCGGTGTTCGGGCTGATGGGCTTACAAATCTATATGGGTGTTCTTAAACAAAGTGC 870  
QY 867 CTGTCGGTGTTCGGGCTTATGATGGGCTACAGATCTATATGGGCTGCTCACCGAGAAGTGC 926  
Db 871 ATTAACGATTTCCCTCGACGGCAGTTGGGCAATCTGACCGATGAAACTGGTTTCTA 930  
QY 927 ATCAAGAAGTTCCCTCGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGACTAT 986  
Db 931 CACAAATAGCAACAGTTCCTCAATTTGTTTACGGAGACGATGCGGAGTATATATCCGGTGTGC 990  
QY 987 CACAAATCGCAATAGCTCCAATTTGTTTATTCGAGGACGAGGCACTCTCATTTCCGTTATGC 1046  
Db 991 GGAATGTATCCGTCGGGCAATGCGCGAAGATTTACGTCTGCTGACGGGCTTCGGC 1050  
QY 1047 GGCATATATCCGTCGGGCAATGCGGACGACGATTAAGTGTGCTGCGCAGGGTTCGTT 1106  
Db 1051 CCAATCCCACTACGACTACACCAATTTTCGACTCATTCGGTTGGGCTTTCCCTGTCGGC 1110  
QY 1107 CCGAATCGGAATATGGCTACACCAAGTTCGATTCGTTCCGATGGGCTTTCCTGTCGCC 1166  
Db 1111 TTTCGTCTCATGACCCAGATTTCTGGAGGATCTGTATACGACGCTGCTGCAAGCAGCT 1170  
QY 1167 TTCCGGCTGATGACACAGGACTTCTGGAGGATCTGTACCAAGCTGTTGCGGCGCGCC 1226  
Db 1171 GGACCTGSCACATGTGTCTTTATAGTATCATCTCTCTAGGTTTCATTTCTATCTTTG 1230  
QY 1227 GGACCATGGCACAATGCTGTCTTTATAGTATCATCTCTCTAGGTTTCATTTCTTTG 1286  
Db 1231 AATTTGATTTTGGCCATTTGCCATGTCTTATGACGAATTTGCAAAAGAGCGCGAAGAA 1290  
QY 1287 AATTTGATTTTGGCCATTTGCCATGTCTGTATGACGAATTTGCAAAAGAGCGCGAAGAA 1346  
Db 1291 GAAGAGCTGCCGAGGAGGCGGATCCGAGAGCTGAAGAGCGGCGACGACCGCAAGCG 1350  
QY 1347 GAAGAGCTGCCGAGGAGGCGGATACGTTGAAGGAGGAGAGCTGCGCGCCCAAGCG 1406  
Db 1351 GCCAACTGGAGGAGCGGCCAATGTAGCAGCTCAAGCGGCTCAGAGTGCAAGCGGATGCC 1410  
QY 1407 GCCAACTGGAGGAGCGGCCAATGGCAGGCTCAGGACGACGAGTACGCGCTGCCGCC 1466  
Db 1411 GCTGCGGAGCTCTGATCCGAGATGGCAAGAGTCCACGCTACTCTGTCAATAGCTAT 1470  
QY 1467 GAAGAGGCTGCACTGATCGGAATTTGGCAAGAGTCCGACGATTTCTTGCATCAGCTAT 1526  
Db 1471 GAAGTGTGTTGGCGGAGAGGCGAACGATGACAAACAAAGGAGAGATGTCGATA 1530  
QY 1527 GAGCTATTTGTTGGCGGAGAGGCGAACGATGACAAACAAAGAGAGATGTCCTAT 1586  
Db 1531 CGCAGGCTCGAAGTGAATCGGAGTCCGGTGGGTTATCAAGAGCAACACGACCTTACC 1590  
QY 1587 CGGAGGCTCGAGTGGAGTCCGAGTCCGTTAGCGTTATACAAAGACCAACGACCTTACC 1646  
Db 1591 ACAGCAC-CC--GCTACTAAGTCCGTAAAGTTAGCAGGCTTCTCTTATCTTACTCTGT 1647  
QY 1647 ACAGCACCAAGCTACCAAGTTCGTAAAGTGTAGCAGGACGATCTCTTATCTTACTCTGT 1706  
Db 1648 TCACCAATTAACCTACGCCGGGATCACGTAGTTTCACACAGGTACACAATACGAATGGG 1707  
|||||

QY 1707 TCACGGTTTAACATACGCGAGGGATCAGTAGTTCTCACAAAGTACACGATACGGAACGGA 1766  
Db 1708 CQTGACGCTTTTGGTATATACAGGTAGCGATCGCAAGCCATTGGTACTGCAACATATCAG 1767  
QY 1767 CQTGCGCCTTTGGTATATACCGGTAGCGATCGTAAGCAATTGGTATTGTCAACATATCAG 1826  
Db 1768 GATGCCACGACGACTTTGCCCTATGCCGATGACTCGGAATGCCGTAAACCAATGTCGAA 1827  
QY 1827 GATGCCACGACGACTTTGCCCTATGCCGACGACTCGGAATGCCGTACCCCGATGTCGAA 1886  
Db 1828 GAGAATGGTGCATATATAGTACCAGCTTACTTGTAAATTTAGTGTTCFAGACATCTTCA 1887  
QY 1887 GAGAATGGGCTCATATAGTGCCTGCTACTATGGCAATCTAGGCTCCGACACTCATCG 1946  
Db 1888 TATACTCGCATCAATCAAGAATCTCTATATACATCACATGTGTATTTATGGGTGGCATG 1947  
QY 1947 TATACTCGCATCAGTCCCGAATATCGTATACCTACATGGCGATCTACTCGGGGCTATG 2006  
Db 1948 GCGGCTATGGTGCAGCAATGACCAATGACCAAGAGAGCAATTCGCGAGTCGCAACACGCG 2007  
QY 2007 GCGGCTATGGGCTCAGCAATGACCAATGACCAAGAGAGCAATTCGCGAGTCGCAACACGCG 2066  
Db 2008 AATCAATCAATCGGTCTGCAACCAATGGTGGCAGTACTAGCGCGGCTGGTGGCTATCCC 2067  
QY 2067 AATCAATCAAT-GG-GC-GCCACCAATGGCGCACAC-CTGTC--TGA--C-A--CC 2114  
Db 2068 GATGCCAATCACAAGAACAAAGGATTAATGAATGGGTGAGGATTTATACAGACCAAGCT 2127  
QY 2115 AATCAACAAGCTC---GATCATCGGACTACGAAATTTGGCTGGAGTGCACGCGCAAGCT 2171  
Db 2128 GCGAAATTAACACACACGACCAATCTTTTATCGAGCCGCTCAAACTCAAACTGTTGTA 2187  
QY 2172 GCGAAATTAACACATCATGACCAATCTTTTATCGAGCCGCTCCAGACCAACAGTGGT 2231  
Db 2188 GACATGAAAGATGTTATGGTCTTAAATGATATCATTTGAACAAGCCGCTGGTCGAGAT 2247  
QY 2232 GATATGAAAGATGTGATGTCCTGAATGACATCATCGAACAGCCGCTGTCGGCACAT 2291  
Db 2248 CGTGTAGTGAACGAGGTG-----AGGACGATGACGAAGAT 2283  
QY 2292 CCGGCAAGCGATCGCGGTGTCCTCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351  
Db 2284 GGTCCACATTTCAAGGACATCGCCCTCGAATATATCTTAAAGGACATCGAAATCTTTGT 2343  
QY 2352 GGGCGGACGTTCAAGACAGGACCTCGAAGTATCTCTCAAGGACATCGATGTTGTTGT 2411  
Db 2344 GTATGGACGTTGTTGGGTGTTGTTAAATTTACGAATGGGTCTCCTTTATTTGTTTC 2403  
QY 2412 GTGTGGGACGTTGCTGGGTTTGGTTGAAATTTTCAAGGAGTGGGTATCGCTCATCTTC 2471  
Db 2404 GATCCATTCGTGGAGCTCTTTCATTCCTGTGTATTTGGTCAATACAAATGTTTCATGGCC 2463  
QY 2472 GATCCCTTCGTGAGGCTCTTCATCACGCTGTGATTTGGTCAACACGATGTTTCATGGCA 2531  
Db 2464 ATGATCATCACGACATGAATCCGGAATTTGAGAAGTGTCTGAAAAGTGTGTAATTTTC 2523  
QY 2532 ATGATCATCACGACATGAACAAGAGATGGAACGCGTCTCAAGAGTGGCAACTATTTTC 2591  
Db 2524 TTACGCGGACTTTTGAATTTAGGCGCAGCATGAACTGATGCGCATGAGCCCGCAAGTAC 2583  
QY 2592 TTCACCGCCACTTTGGCATTCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTAC 2651  
Db 2584 TACTTCAGGAAGGCTGGAACATTTTCGATTTTCAATTTTGGCTTGTCTCTGCTGGAA 2643  
QY 2652 TATTTACGAGGCTGGAACATCTTCGACTTCATTCGTGGCCCTATCGCTATTGGAA 2711  
Db 2644 TTGGCCCTGGAGGTGTCAGGGCTCTCGGTGTGAGAAGTGTTCGTTGCTTCGTGTA 2703  
QY 2712 CTGGGACTCGAGGCTGTCAGGGTCTCTCGGTATTCGGTCTTCGATTTGCTGCTGTA 2771  
Db 2704 TTCAAATTTGCAAAATCATGCGCCACACTGAATTTTACTCATTTTCGATTTGCGCGGACA 2763  
QY 2772 TTCAACTGGCCAAAGTCTTGCCCCACACTTAATTTTACTCATTTTCGATTTGCGGACGACC 2831





Db 511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 570  
QY 567 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 626  
Db 571 TTCATTTTATGCGCGTTACGTATCTTAGAGATGCAATGGAATGGCTGGACTTCGTAGTA 630  
QY 627 TTCATTTTATGCGCGTTACGTATCTTAGAGATGCAATGGAATGGCTGGACTTCGTAGTA 686  
Db 631 ATAGCTTTATGTTAGTACCATGGGCATAGATTTAGGTAATCTCGACGTTTGAACA 690  
QY 687 ATAGCTTTATGTTAGTACCATGGGTATAGATTTAGGTAATCTAGCAGCCCTGCGAAGC 746  
Db 691 TTTAGGTTACTGGAGCTCTGAACCGTAGCCATGTGCGCAGGTCTAAAAACCATTTGTC 750  
QY 747 TTTAGGTTGCTGGAGCGCTTAAACCGTAGCCATGTGCGCAGGCTTGAAGACATCGTC 806  
Db 751 GGTGCTGTCATTTGAATCTGTAAAAATCTACGCGATGTGATATTTTGACAAATGTTTTCC 810  
QY 807 GCGCGCTCATCGAATCGGTGAAGATCTCGCGATGTGATATCTTGACCATGTTCTCC 866  
Db 811 CTGTGCGTGTTCGCGTGTATGGCCCTACAAATCTATATGCGTGTCTTAACACAAAAGTGC 870  
QY 867 CTGTGCGTGTTCGCGTGTATGGCCCTACAGATCTATATGCGCGTGTCTACCGAGAAGTGC 926  
Db 871 ATTAACGATTTCCCTGGAGCGAGTTGGGCAATCTGACCCATGAAAACCTGGTTCTTA 930  
QY 927 ATCAAGAAGTTCCCGTGGACGTTCTCGTGGCAATCTGACGACGAGAACTGGGACTAT 986  
Db 931 CACAATAGCAACAGTTTCCAATGGTTTACGGAGAAGATGGCGAGTCATATCCGGTGTGC 990  
QY 987 CACAATCGCAATAGTCCCAATGGTATTCGAGGACGAGGCGATCTCATTTCCGTTATGC 1046  
Db 991 GGAATGTATCCGTTGGGACAAATCGGCGAGGATACGTCTGCTGCGAGGCTTCGGC 1050  
QY 1047 GGCAATATATCCGTTGGGGAATCGGACGACGATTAACGTGTGCTGCGAGGCTTTGGT 1106  
Db 1051 CCNAATCCCAACTACAGCTACACAGTTTCGATTCATTCGGTTGGGCTTCCCTGTGCGG 1110  
QY 1107 CCGAATCCGAATATGGCTACACAGCTTCGATTCGTTGCGTGGGCTTCCCTGTGCGGC 1166  
Db 1111 TTTGCTCTATGACCCAAAGATTTCTGGAGGATCTGTATCAGCAGCTGCTGCAAGCAGCT 1170  
QY 1167 TTCGGCTGATGACAGAGACTTCTGGAGGATCTGTACCAGCTGGTGTTCGCGCGGCC 1226  
Db 1171 GGACCTTGGCACATGTTGTTTATAGTTCATCATCTCTTAGGTTCAATCTATCTTGTG 1230  
QY 1227 GGACATGGCACATGCTGTTCTTTATAGTTCATCATCTCTTAGGTTCAATCTATCTG 1286  
Db 1231 AATTGATTTGGCCATGTTGCCATGTCTTTATGACGAATTCCAAAGAGCGCGAAGAA 1290  
QY 1287 AATTGATTTGGCCATGTTGCCATGTCTGTATGACGAATTCCAAAGAGCGCGAAGAA 1346  
Db 1291 GAAGAGCTCCGAGGAGGCGGATACGAGAGCTGCAAGAAGCGCAGCAGCAAGGCG 1350  
QY 1347 GAAGAGCTCCGAGAGGAGGCGGATACGTTGAAGCGGAAGAAGCTGCCGCGCCAAGCG 1406  
Db 1351 GCCAACTGGAGGAGCGGGCCAATGTAGCAGCTCAAGCGCTCAGGATCAGCGGATGCC 1410  
QY 1407 GCCAAGCTGGAGGAGCGGGCCAATGCCAGGCTCAGCAGCAGCGGATCGGCTCGCGCC 1466  
Db 1411 GCTGCGGCACCTCTGCATCCCGAGATGGCAAGAGTCCCAAGTACTCTTGCATAGCTAT 1470  
QY 1467 GAAGAGCTGCATGTCATCGGGAATGGCCAAAGAGTCGACGATTTCTTGCATCAGCTAT 1526  
Db 1471 GAAGTGTTCCTGGCGGAGAGGCGCAAGATCACAACACAAAGAGAGATGTCCATA 1530  
QY 1527 GAGCTATTTGTGGCGGAGAGGCGCAAGATGACAAACAAAGAGAGATGTCCATT 1586  
Db 1531 CGCAGCTCGAAGTGAAGTCGGAGTCGGTGAGCGGTTATACAAAGACAAACAGCACCTACC 1590  
QY 1587 CGGAGCTCGAGGTGGAGTCGGAGTCGGTGAGCGGTTATACAAAGACAAACAGCACCTACC 1646  
Db 1591 ACAGCAC-CC--GCTACTAAAGTCCGTCAAAGTTAGCACGACTTCTCTTATCCTTACCTGGT 1647

QY 1647 ACAGCACACAAAGCTACCAAAGTTCGTTAAAGTGAGCACACATCTCTTATCTTACCTGGT 1706  
Db 1648 TCACCATTTTAACTACGCGCGGATCACGTAGTTTACACAAAGTACACAAATGCAAAATGGG 1707  
QY 1707 TCACCGTTTAAATACGACGAGGATCACGTAGTTTTCACAAAGTACACGATACGGAACGGA 1766  
Db 1708 CFTGGACGTTTTGGTATACCAAGTACGATCGCAAGCCATTTGGTACTGCAAAATATCAG 1767  
QY 1767 CFTGGCGGTTTTGGTATACCCGCTAGCGATCGTAAGCCATTTGGTATTTGTCAACATATCAG 1826  
Db 1768 GATGCCACACGATTTGGCTTATGCCGATGACTCGAATGCCGTAAACACCAATGTCGGA 1827  
QY 1827 GATGCCACACGATTTGGCTTATGCCGATGACTCGAATGCCGTAAACACCAATGTCGGA 1886  
Db 1828 GAGAATGGTGCCATTTAGTACCAAGCTTACTATTGTTAAATTTAGGTTCTAGACATTTCTTA 1887  
QY 1887 GAGAATGGGCGCATCATAGTGCCTGTACTATGGCAATCTAGGCTCCCGACACTCATCG 1946  
Db 1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGTATTTATGGGTGCGATG 1947  
QY 1947 TATACCTCGCATCAAGTCCCGAATATCGTATACCTACATGGCGATCTACTCGGCGCATG 2006  
Db 1948 GCGGCGATGGGTGCCAGCACAAATGACCAAGAGAGCAAAATGGCGAGTGCACACACGC 2007  
QY 2007 GCGGCGATGGGCGTCAGCAAAATGACCAAGAGAGCAAAATGGCGAAGCGCAACACGC 2066  
Db 2008 AATCAATCAATCGGTGCTGCAACCAATGGTGAGTACGGCTGGTGGTGGCTATCCC 2067  
QY 2067 AATCAATCAGT--GG-CC-CCCAATGGCGGACCA---C--CTG-TC-TGGACA--CC 2114  
Db 2068 GATGCCAATCACAAGGAACAAAGGATTTATGAAATGGGTGAGGATTTATACAGACGAGCT 2127  
QY 2115 AATCACAAGCTC---GATCATCGGACTACGAAATTTGGCTGGAGTGCAGGACGAGCT 2171  
Db 2128 GCGCAAAATTAACACACACACAAATCTCTTTATCGAGCCCGTCCAAACTCAACAGTGGTA 2187  
QY 2172 GCGAAGATTAAACATCATGACAAATCTTTATCGAGCCCGTCAGACACAAAGCGTGT 2231  
Db 2188 GACATCAAGAGATTTATGGCTTAAATGATCATTTGAACAGCCCGCTGGTGGCATAGT 2247  
QY 2232 GATATGAAGATGTGATGGTCTGTAATGACATCATCGAACAGCCCGCTGGTGGCACAGT 2291  
Db 2248 CFTGCTAGTGAACGAGGTG-----AGGACGATGACGAGAT 2283  
QY 2292 CGGCAAGCATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGGACGATGACGAGAT 2351  
Db 2284 GGTCCACATTTCAAGACATCGCCCTCGAATCATCTCTAAAAGGCATCGAAATCTTTGT 2343  
QY 2352 GGGCCGACGTTCAAAGACAAGGCACCTCGAAGTGATCTCTCAAAGGCATCGATGTGTTGT 2411  
Db 2344 GTATGGGACTGTTGTTGGTGGTTAAAAATTCAGGAATGGGTGCTCTTATTTGTTGTTTC 2403  
QY 2412 GTGTGGGACTGTTGCTGGGTTGGTTGAAATTTTCAGAGATGGGTATCGCTCATCGTCTTC 2471  
Db 2404 GATCCATTCGTGGAGCTCTTCATTTACCTGTGTTATTTGGTCAATACGATGTTTATGGCC 2463  
QY 2472 GATCCCTTCGTGAGCTCTTCATCGCTGTGCAATTTGGTCAACAGATGTTTCATGGCA 2531  
Db 2464 ATGGATCATCAGACATGAATCCCGAATTTAGAGAAGGTGCTGNAAGAGTGTAACTATTTTC 2523  
QY 2532 ATGGATTCACACGATATGAACAGGAGATGGAAAGCGCTCTCAAGAGTGGCACTATTTTC 2591  
Db 2524 TTCACGGCCACTTTTCGATTTGAGGCCAGCATGAAACTGATGGCCATGAGCCCGAAGTAC 2583  
QY 2592 TTCACGCCCACTTTTCCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCAAGTAC 2651  
Db 2584 TACTTCCAGGAAGGCTGGAACATTTTCGATTTTCATTTATTTGGCTTGTCTCTGCTGGAA 2643  
QY 2652 TATTTCCAGGAGGCTGGAACATCTTCGACTTCATTTATCGTGGCCCTATCGCTATTTGGA 2711  
Db 2644 TTGGGCGCTGGAGGCTGTCCAGGCGCTCTCGGTTTGAGAAAGTTTTCGTTTGTCTCGTGA 2703

QY 2712 CTGGAGCTCGAGGGTGTCCAGGGTCTGTCCGATATTCGCTTCCCTTTCGATTGCTGGGTGTA 2771  
Db 2704 TTCAAAATGGCAAAATCATGGCCCACTGAATTTACTCATTTTCGATTTAGGCGCGACA 2763  
QY 2772 TTCAAACTGGCCAAAGTCTTTGGCCACACTTAATTTACTCATTTTCGATTTAGGACGCACC 2831  
Db 2764 ATGGGTGCATTTGGTGAATCTGACATTTGTACTTTGGATTATCATCTTCATCCCTCCGCTG 2823  
QY 2832 ATGGCCCTTTGGGTAACTGTGACATTTGTACTTTGGATTATCATCTTCATCTTCATCTTGGGTTG 2891  
Db 2824 ATGGGAATGCAACTTTTCGGAAGACCAATTAATGACCAAGGATCGCTACAAAGACCAAT 2883  
QY 2892 ATGGGAATGCAACTTTTCGGAAGAAATTAATCATGATCACAAGGACCGCTTTCGGATGCG 2951  
Db 2884 GAATTTGGCGGCTGGAAATTTACGGACTTCATGACAGACTTCATGATTTGTTTCCAGATG 2943  
QY 2952 GACCTGGCGGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATTCGTTTCCGGGTTG 3011  
Db 2944 CTGTGGGAGAGTGCATCGAGTCCATCTGGGACTTGCATGTAATGTGGCGGATGTCAGCTGT 3003  
QY 3012 CTGTGGGAGAAATGATCGAGTCCATGTGGGACTGCAATGTAATGTGGCGGATGTCGTGCG 3071  
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QY 3072 ATTCCTCTTCTTTGGCCACCGTTGTATCGGCAATCTTGTGGTACTTAACCTTTCTTA 3131  
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QY 3132 GCTTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCGGATACGAT 3191  
Db 3124 ACCAATAAAATAGCAGAGGCTTCAATCGTATTCCTCGTTTAAAGAACTCGGTGAAACGT 3183  
QY 3192 ACGAATAAAATAGCGAGGCTTCAATCGAATTTGGCCGATTTAAAGTTTGGTAAAGCGT 3251  
Db 3184 AATATTGCCGATGTTGTTAAAGTTAAATTCGAAATAAATGACAAATCAAAATAGTGACAA 3243  
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Db 3244 CCATCAG-----A-CA-----TGG--CGAT-A--ATG----- 3265  
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QY 3372 GAACCTGGAGCTGGGCCACGACGAGATCTCCGCCGACGCCCTCAAGAAGGGGATCAAG 3431  
Db 3325 GCGAGACCCAGCTGGAGTGGCCATTTGGCGATGGCATGGAGTTTCAGATACATGCGCGAT 3384  
QY 3432 GAGCAGACGCACTGGAGGTGGCCATCGGGATCGGATGGGAATTCACGATACACGGCGAC 3491  
Db 3385 ATGAAAACCAACAAAGCCCAAGAAATCAAAATTCATPAAACACAAACGATGATTGGAAC 3444  
QY 3492 ATGAGAACCAACAGCCGAGAAATCCAAATATCTAATTAACGCAACGATGATTGGCAAC 3551  
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QY 3552 TCAATTAACCCCAAGACAATAGATGGAACACGAGCTTAAACCATAGAGGTTTGTCTTTA 3611  
Db 3505 CAGGACGATGACACTGCCAGCATTAACATCATATGCTAGCCATTAAGAATCGACCATCAAG 3564  
QY 3612 CAGGACGACGACACTGCCAGCATTAACATCATATGCTAGCCATTAAGAATCGACCATCAAG 3671  
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QY 3672 GACGAGAGCCACAAGGCGACGCCAGACCATTCGAGGGCGAGGAGAAACGGGACGTCAGC 3731  
Db 3625 AAGAGGACCTCGGCTTCACGAGGACTTGGACGAGGAGGCGCGAGGCGCATGAGGCGCAG 3684  
QY 3732 AAGGAGGATTTAGGCTTCGACGAGGAACCTGGACGAGGAGGCGCATGCGAGGAGGCGCG 3791  
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QY 3792 CTCGACGGTGATCATATTTATTCATGACA---CGACGAGGATATCTCGATGAATATCCA 3848

Db 3745 GCCGACTGTTTCCCGACTCGTACTACAAGAAATTTCCGATCTTGGCCGCGCAGGAGAC 3804  
QY 3849 GCTGATTGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGCTAGCATGAC 3908  
Db 3805 TCGCCGTTCTGGCAAGATGGGGCAATTTACGACTGAAACTTTTCAATTAATTAATGAAAT 3864  
QY 3909 TCGCGGTTCTGGCAAGATGGGGCAATTTACGACTGAAACTTTTCAATTAATTAATGAAAT 3968  
Db 3865 AAATATTTTGAAACCGGAGTTATCATTATGATAGTAGCTTAGCTTTGGCCCTTA 3924  
QY 3969 AAATATTTTGAAACAGCTGTTATCATTATGATTTATGATAGCTTAGCTTTGGCATT 4028  
Db 3925 GAAGATGTTCTTTACCGGATCGACCTGTCTCATGAGGATATATTTACTACATGGACAG 3984  
QY 4029 GAAGATGTACATCTGCCACAAAGACCCATCTGCAGGATATTTTATATATATGACAGA 4088  
Db 3985 ATATTACGGTGATATCTTTTGGAGATGTTGATCAATGTTGGCCCTGGGCTTTAAG 4044  
QY 4089 ATATTACGGTGATATCTTTTGGAAATGTTAATCAAGTGGTTGGGCTCGGCTTCAA 4148  
Db 4045 GTTACTTTCAACAATGCTGTGTGGCTGATTTTCGATTTTCGATTTGCTATGCTTATA 4104  
QY 4149 GTGACTTTCAACAAGCGCTGTGTGGCTCGATTTTCGATTTGCTATGCTTATC 4208  
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QY 4209 AACTTCGTTGCTTCACTTGTGGAGCTGGTGTATTTCAAGCCTTCAAGACTATCGAACG 4268  
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QY 4269 TTAAGAGCACTGAGACCACTAGTGCCCATGTCCTGATGAGGGCATGAGGGTCTGCT 4328  
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QY 4329 AATGGCTGTTTCAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGCTAATATT 4388  
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QY 4509 GAGAACTACAGCTGGGTGAATTCAGCAATGAATTTTCGATCATAGTAAACGCTATCTG 4568  
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QY 4689 GTATTCTTCATTAATTTGGATCATTTTTCACACTCAATCTGTTTCAATGTTGTTATCAT 4748  
Db 4645 GATAATTTTAAACAACAAAGAAAGCAGGTTGATCATTAGAAATGTTTCATGACAGAA 4704  
QY 4749 GATAATTTTAAAGCAAAAGAAAGCAGGTTGATCATTAGAAATGTTTCATGACAGAA 4808  
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QY 4809 GATCAGAAAAAGTACTATATGCTATGAAAGATGGGCTCTAAAAACCATTTAAAGGC 4868  
Db 4765 ATTCCAGACCGGAGTGGCCACCAAGCAATAGTATTGCAATAGCTTACAGATAAAAA 4824  
QY 4869 ATTCCAGACCAAGGTGGCCACCAAGCAATAGTATTGCAATAGCTTACAGATAAAAA 4928



D	b	4825	TTCGATATAAATCAATTAGTTGTTCATATGGCTTAAACATGTTTTACCATGACCCCTCGATCGG	4884
Q	y	4929	TTCGATATAAATCAATTAGTTATTCATTTGGTGTGAACATGTTTCAOCATGACCCCTCGATCGT	4988
D	b	4885	TACGACGCCTCCGAGGCGTPACAACAATGTCCTCGACAACATCAATGGGATATTCGTAGTT	4944
Q	y	4989	TACGATCGCTCGGACACGTAATACCGCGTCTTAGACTATCTCAATGGCATATTCGTAGTT	5048
D	b	4945	ATTTTCAGTGCGGAATGCTCTATTAAAAATATTTCGGCTTTACGATATCACTATTTCAAAG	5004
Q	y	5049	ATTTTCAGTTCGGAATGCTCTATAAAAATATTTCGGCTTTACGATATCACTATTTATTGAG	5108
D	b	5005	CCATGGAATTTATTGATGATGATGCTAGTTGTCTATTTATCCATCTTAGGCTTGTACTTACG	5064
Q	y	5109	CCATGGAATTTATTGATGATGATGCTAGTTGTCTATTTATCCATCTTAGGCTTGTACTTACG	5168
D	b	5065	GACATCATTTGAGAAGTATTTCCGTATTCGCCGACATGCTCCGCTGGTGAGAGTGGCCAAA	5124
Q	y	5169	GATATTTCGAGAAGTACTTCGTGTCCGCGACCTGCTCCGAGTGGTGCTGGTGGCGAAA	5228
D	b	5125	GTGGGTGCTGTCTCCTCGGTTTAGTCAAGGGTGCCAAGGATATCCGGAAGTTGCTGTTCCGG	5184
Q	y	5229	GTGGCGCGTCTCTCGACTGTGTGAAGGAGCCCAAGGSCATTCGACACATGCTCTCTCGG	5288
D	b	5185	TTAGCCATGTGCTGTGCTGCCCTTATTCAACATTTGTCTGTGTTGCTGTTCTTTGGTGATGTT	5244
Q	y	5289	TTGGCCATGTGCTGTCCGCGCCCTGTTTCAACATCTGCCTGCTGCTTCTTGGTCAATGTT	5348
D	b	5245	ATCTTTTGCTATCTTTGGCATGTCTCTTTCATGTCATGTCAAGAGAGAGAGCGGCAATAAT	5304
Q	y	5349	ATCTTTGGCAATTTTGGGCATGTGGTCTTCAATGACGTTGAAGGAGAGAGCGGCATTAAC	5408
D	b	5305	GCTGTGTATAATTTTAAGACATTTGCCCAAAGTATGATATGCTGTTTTCAGATGCTCAACC	5364
Q	y	5409	GAOGTCTACAACCTTCAAGACCTTTGGCCAGACATGATCCTGCTCTTCAGATGTCGAAG	5468
D	b	5365	TCAGCCGTTTGGAGTGGTGTGTAGATGCCATPATAATCAATGAGGAAGATTTGGATCCACCC	5424
Q	y	5469	TCAGCCGTTTGGAGTGGTGTACTTGGACGCCATPATAATGAGGAAGCATGCGATCCACCC	5528
D	b	5425	GACAACGACAAGGCTATCCGGGCAATTTGGTGTTCAGCGACTGTTGGAATTTACGTTTCTC	5484
Q	y	5529	GACAGGCAACAAGGCTATCCGGGCAATTTGGTGTTCAGCGACGTTTGGAAATCAACGTTTCTC	5588
D	b	5485	CTTTTCATCTAGTTATAAGCTTTTGTAGTATTATAATGTACATTCGTGTCATTCCTC	5544
Q	y	5589	CTCTCATACCTAGTTATAGCTTTTGTAGTATTATAATGTACATTCGTGTCATTCCTC	5648
D	b	5545	GAGAACTATAGCCAGGCTACGAGGATGTACAGGAGGTCTCACCGACGACGATTTACGAT	5604
Q	y	5649	GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGCTTAACCGACGACGACTACGAC	5708
D	b	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGCGACCCAGTACATACGCTACGAC	5664
Q	y	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCGACCCAGTACATACGCTATGAT	5768
D	b	5665	CACGTGTCGAGTTCTGACGCTGTGGAGCGCGCTGCGAGATCCCAACGCCAACAAG	5724
Q	y	5769	CACGTGTCGGAATTCCTGGACGCTACTGGAGCCCCCGCTGCGAGATCCCAACGCCAACAAG	5828
D	b	5725	TACAAAATCATATCGATGGACATGCCGATATGTCGGGGCGACATGATGACTGTGTGGAT	5784
Q	y	5829	TACAAGTACATATCGATGGACATACCCATCTCTCGGGTGACCTCATCTACTGCGTCGAC	5888
D	b	5785	ATATTGATGCCCTGACCAAGGACTTTCTTTTGGCGCGAAGGGTAATPCGATCCGAGGAGACG	5844
Q	y	5889	ATCTCTGACGCCCTTACGAAAGACTTCTTTTGGCGGGAAGGGCAATCCGATAGAGGAGACG	5948
D	b	5845	GGTGAATTTGGTCAGATACGGCGGACCGGACCCGAGGATATGATCCGGTCTCGCTCG	5904
Q	y	5949	GGTGAGATTTGGTGAGATACGGCGGCCCGCGGATACGGAGGGCTACGAGCCCCTCTATCA	6008
D	b	5905	ACACTGTGGCGCCAGCGGTGAGGAGTACTGCGGCCAAAGCTGATACAGAATTCGCTGGCG	5960

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QY 6009 ACAGTGTGGCGTCAGCGTGAGGAGTACTGCGCCGCGCTAATCCAGCAGCGCTGGCG 6064
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RESULT 10
ID US-08-608-618-2 STANDARD; DNA; UNC; 6318 BP.
AC xxxxxx
DT
Sequence 2, Application US/08608618
DE Sequence 2, Application US/08608618
CC GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Knipple, Douglas C.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
CC TITLE OF INVENTION: HOUSE FLIES
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: P.O. Box 1051, Clinton Square
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/608,618
CC FILING DATE:
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Timian, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6318 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA
CC SEQUENCE 6318 BP; 1713 A; 1349 C; 1592 G; 1664 T; 0 OTHER.
Query Match 56.2%; Score 3660; DB 19: Length 6318;
Best Local Similarity 84.7%; Pred. No. 0.00e+00;
Matches 4978; Conservative 0; Mismatches 814; Indels 84; Gaps 21;
Db 151 ATACGATATGATGACGAGGACGGAAGTGCACACGCGGATCCACACACTTGAACAG 210
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QY 207 ATCCGATATGATCAGGAGCGAGGATGAAGTCCACACCGGATCCTTACACTTGAACAG 266
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Db 211 GGTGTGCTATACCTGTTGCAATGACGAGGCAGCTTCCCGCCGGAAFTGGCTCCACATCCT 270
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Db 331 AAGCATATTTTTCGTTTTTCTGCTCAAAAGCAATGTGGCTCTCGATCCCAATTCAG 390
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QY 387 AAAGATATTTTTCGTTTTTCTGCTCAAAAGCAATGTGGCTCTCGATCCCAATTCAG 446
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Db 391 ATACGTCGTAGTACATTTAATTTTAGTGCATCCCTGTTTTTTCGTTAATCATTAATCACC 450
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QY 447 ATAGTCGTGTGGCCATTTACATTTCTAGTGCATCATTAATTTTCCCTATTTCATCATCACC 506
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Db	451	ACTATTCCTAACTAATTTGTAATTTTAAATGATATGTCGCGACACGCCCGCTCGAATCCACA	1531	CGCAGCGTCGAAAGTGGAAATCGGAGTCGGTAGCGGTATACAAAGACAAACACGACCTACC	1590
Qy	507	ACAAATCTCGTCAACTGCATCTGATGATATGCGGACAAACGCCCGGTGAGTGCACCT	1587	CGGAGCGTCGAGGTGGAGTCGGAGTCGGTACGCGTTATACAAAGACAAACACGACCTACC	1646
Db	511	GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT	1591	ACAGCAC-CC--GCTACTAAAGTCCGTCAAGTTAGCAGGACTTCCTTATCTTACCTGGT	1647
Qy	567	GAGTGATATTCACCGGAACTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT	1647	ACAGCACACCAAGCTACCAAAGTTCTAAAGTGAGCAGGACATCCTTATCTTACCTGGT	1706
Db	571	TTCAATTTATCCCGTTFACGTAATCTTAGAGATGCATGGAATTGGCTGGACTTCGTTAGTA	1648	TCACCAATTTAACTACGCGGGGATCAGTAGTTTACACAAGTACACAATACGAAATGGG	1707
Qy	627	TTCAATTTATCCCGTTFACGTAATCTTAGAGATGCATGGAATTGGCTGGACTTCGTTAGTA	1707	TCACGCTTTAAATACGAGGGGATCAGTAGTTTCTACAAGTACACGATACGGAACGGA	1766
Db	631	ATAGCTTTAGCTTATGTGACCATGGCATAGATATTTAGTAAATCTCGCAGCTTTGAGAAACA	1708	CGTGGACGTTTTGGTATACCAAGTAGCGATCGCAAGCAATTTGGTACTGCAAAACATATCAG	1767
Qy	686	TTCAATTTATCCCGTTFACGTAATCTTAGAGATGCATGGAATTGGCTGGACTTCGTTAGTA	1767	CGTGGCGCTTTGGTATACCGGTAGCGATCGTAAGCCATTTGGTATTTGTCACATATCAG	1826
Db	690	ATAGCTTTAGCTTATGTGACCATGGCATAGATATTTAGTAAATCTCGCAGCTTTGAGAAACA	1768	GATGCCACGACGATTTGCCCTATGCCGATGACTCGAATGCCGTAAACACCAATGTCCGAA	1827
Qy	746	ATAGCTTTAGCTTATGTGACCATGGCATAGATATTTAGTAAATCTCGCAGCTTCGCAAGC	1827	GATGCCACGACGATTTGCCCTATGCCGATGACTCGAATGCCGTAAACACCAATGTCCGAA	1886
Db	750	TTTAGGCTACTGCGAGCTCTGAAACCGTAGCCATTTGTCAGGCTTAAAAACCAATGTCT	1828	GAGAATGGTGCCATTTAGTAGCAGCCTACTATTGTAAATTTAGGTTCTAGCAATCTTCA	1887
Qy	806	TTTAGGCTACTGCGAGCGCTTAAACCGTAGCCATTTGTCAGGCTTAAAAACCAATGTCT	1887	GAGAATGGTGCCATTTAGTAGCAGCCTACTATTGTAAATTTAGGTTCTAGCAATCTTCA	1946
Db	810	GGTGTGTCATTTGAATCTGTAATAAATCTACCGATGTGATATTTGACAAATGTTTTCC	1888	TATACCTCGATCAATCAAGAATCTCGTATACATACATCGGTGATTTATTTGGTGGCATG	1947
Qy	866	GGCGCGCTCATCGAATCGGTGAAGAATCTGCGCATGTGATTTATCCTGACCATGTTCTCC	1947	TATACCTCGATCAATCAAGAATCTCGTATACATACATCGGTGATTTATTTGGTGGCATG	2006
Db	870	CTGTCGGTGTTCGCGCTGATGGGCTACAAATCTATATGGGTGTTCTAAACACAAAGTGC	1948	CGCGCATGGTGCCAGCACAATGACCAAGAGAGCAAAATTTGGCAGTGCACACACACGC	2007
Qy	926	CTGTCGGTGTTCGCGCTGATGGGCTACAAATCTATATGGGTGTTCTAAACACAAAGTGC	2007	GCGCATGGTGCCAGCACAATGACCAAGAGAGCAAAATTTGGCAGTGCACACACACGC	2066
Db	930	ATTAACGATTTCCCTCGACGGCAGTTGGGCAATCTGACCGATGAAATCGTTTCTA	2008	AATCAATCAATCGGTCTGCAACCAATGGTGGCAGTAGTACGGCCGGTGGTGGCTATGCC	2067
Qy	986	ATCAAGAAATTTCCCTCGACGGTTCCTGGGCAATCTGACCGAGAGAACTGGGACTAT	2067	AATCAATCAATCGGTCTGCAACCAATGGTGGCAGTAGTACGGCCGGTGGTGGCTATGCC	2114
Db	990	CACATAGCAACAGTTCCAATTTGGTTTACGAGAACGATGCGGATCATATCCGCTGTC	2068	GATGCCAATCACAAGGACAAAGGGATTTATGAATGGGTTCAGGATTTATACAGACGAAGCT	2127
Qy	1046	CACATAGCAACAGTTCCAATTTGGTTTACGAGAACGATGCGGATCATATCCGCTGTC	2115	AATCACAAGTCT---GATCATCGGACTACGAAATTTGGCTGGAGTGCAGGACGAAGCT	2171
Db	1050	GGAAATGATTCGGGTGCGGACAAATCCGCGAAGATTAAGTCTGCTGCGCTCAGGGCTTCGCG	2128	GGCAATAATAAACACACACGACAAATCTTTTATCGAGCCGCTCCAAACTCAAAACAGTGGTA	2187
Qy	1106	GGCAATATATCCGTTGCGGGCAATCCGACGACGATTAAGTCTGCTGCGCTCAGGGTTCGCT	2172	GGCAAGATTTAAACATCATGACAATCTTTTATCGAGCCGCTCCAGACACAAACGGTGGT	2231
Db	1110	CCCAATCCCAACTAGACTACACAGTTTCGACTCATTTCCGTTGGCTTTCCTGTCGCGC	2188	GACATGAAAGATGTTATGGTCTTAAATGATATCATTTGAACAACCCGCTGGTGGCATAGT	2247
Qy	1166	CGAAATCCGAATTTAGCTTACCAAGTTCGATTCGTTGGATTCGTTGGCTTTCCTGTCGCGC	2232	GATATGAAAGATGTTATGGTCTTGAATGACATCATCGAATCGGCTGGTGGCAGAGT	2291
Db	1170	TTTCGCTCATGACCAAGATTTCTGGGAGGATCTGATCAGCAGCTGCTGCAAGCAGCT	2248	CGTCTAGTGAACGAGGTG-----AGGACGATGACGAAGAT	2283
Qy	1226	TTCCGCTCATGACACAGGACTTCTGGGAGGATCTGACCACCTGGTGTGGCGCGCGC	2292	CGGCAAGCGATCGCGGTCTCCGTTTACTATTTCCTCAACAGGAGCGATGACGAGAT	2351
Db	1230	GGACCTGGCACATGTTCTTTATAGTCATCATCTTCCTTAGGTTCAATTCATCTTTGTG	2284	GGTCCCACTTCAAGGACATCGCCCTCGAATATATCTTAAAGGATTCGAAATCTTTTGT	2343
Qy	1286	GGACCATGGCACATGTTCTTTATAGTCATCATCTTCCTTAGGTTCAATTCATCTTTGTG	2352	GGGCGGAGTTCAAAGACAAAGGCACTCGAAGTGTATCTCTCAAGGCAATCGATGTTTGT	2411
Db	1290	AAATTTGATTTGGCCATTTGTCCTATGACGAATTCGAAAGAGGCCCGCAAGAA	2344	GTATGGACATGTTGTTGGGTGGTGGTAAATTTTCAGGAATGGTCTCTTATTTGTTTC	2403
Qy	1346	AAATTTGATTTGGCCATTTGTCCTATGACGAATTCGAAAGAGGCCCGCAAGAA	2412	GTGTTGGGAGTGTTCCTGGGTGGTGGTAAATTTTCAGGAGTGGGTATCGCTCATCGTCTTC	2471
Db	1350	GAAGAGGCTGCCGAGGAGGCGATCCGAGAGCTGAAAGAGCGGACGACGCCAAGGCG	2404	GATCCATTTGGTGGAGCTCTTCATTACCCCTGTATTTGGTTCATATCAATATGTTTCATGGCC	2463
Qy	1406	GAAGAGGCTGCCGAGGAGGCGATCCGAGAGCTGAAAGAGCGGACGACGCCAAGGCG	2472	GATCCCTTCGTCGAGCTCTTCATCACCGCTGTGCATTCGTTGGTCAACAGATGTTTCATGGCA	2531
Db	1410	GCACAACTGGAGAGGCGGCAATTTAGCAGCTCAAGCGGCTCAGGATCGCGGATGCC	2464	ATGATCATCATCAGACATGAATTCGCAATTAGAGAAAGTGTGAAAAGTGGTAACTATTTTC	2523
Qy	1466	GCCAAGCTGGAGGAGGCGGCAATGGCAGGCTCAGGACGACGCGGATCGCGCTGCCGCG	2532	ATGGATCACCAGATATGAACAAGGAGATGGAACGCGTCTCAAGAGTGGCAACTATTTTC	2591
Db	1470	GCTGGCGCAGCTTCGATCCGAGATGGCAAGAGTCCCAAGTCTTCCTTAGGCTTACGAT	2524	TTCCAGGCGCACTTTTGCAAATTTGAGGCCAGGATGAACTGATGGCCATGAGCCCCAGTAC	2583
Qy	1526	GAAGAGGCTGCATTCGATCGGAAATTTGGCCAGAGTCCGACGTTATTTTGCATCAGCTAT	2592	TTCCAGGCGCACTTTTGCAAATTTGAGGCCAGGATGAACTGATGGCCATGAGCCCCAGTAC	2651
Db	1530	GAACTGTTTGTGGCGCGAGAGGCGACGATGACAAACAAAGAGAGAGATGTGCGATA	2584	TACTTCCAGGAAGGCTGGAAACATTTTCGATTTCAATTTATTTGGCCCTTGTCTCTCGTGAA	2643
Qy	1586	GAGCTATTTGTTGGCGCGAGAGGCGACGATGACAAACAAAGAGAGAGATGTGCGATT			

Qy	2652	TATTTCAGAGGCGTGGAAACA	TCTTCGACTTCATTA	TCGTGGCCCTATCGCTA	TTGGAA	2711
Db	2644	TTGGCCTCGAGGCTGTC	CAGGCCCTGTCGGTGTTGAGAAGTTTTTCGTTCTCTCGTGTA	2703		
Qy	2712	CTGGACTCAGGCTGTC	CAGGCTGTCGGTATTGCGTTCTCTTCGATTGCTCGTGTA	2771		
Db	2704	TTCAAAATTGC	AAAATCATGGCCCACACTCAA	TTTACTCATTTTCGATTATGGCGCGACA	2763	
Qy	2772	TTCAAACTGGCCAAGTCT	TGGCCACACTTAATTTACTCA	TTTCGATTATGGAGCGACC	2831	
Db	2764	ATGGGTGCATTGGGTAA	CTCGACATTGTACTTTTGCATNTCACTTCATCTTTGCCGTG	2823		
Qy	2832	ATGGCGCCTTTGGGTAA	CTCGACATTGTACTTTTGCATNTCACTTCATCTTTGCCGTG	2891		
Db	2824	ATGGGAATGCAACTTTT	CGGAAGAAGTAATATTGACCA	AAGGATCGCTTCAAGGACCAT	2883	
Qy	2892	ATGGGAATGCAACTGT	TGGGAAGAATAATCAATGATCAC	AGGACCGCTTCCGGATGGC	2951	
Db	2884	GAAATACCGCGCTGGA	ACTTCACCGACTTCATGCACAGCTTCATGATGTGTC	CCGAGTG	2943	
Qy	2952	GACCTGCGCGCTGGA	ACTTCACCGACTTTATGCACAGCTTCATGATGTGTC	CCGAGTG	3011	
Db	2944	CTGTGCGGAGAGTGG	ATCGAGTCCATGTGGGACTGCGATGTATGTGGCGGATGT	CAGCTGT	3003	
Qy	3012	CTCTGCGGGAATTGG	ATCGAGTCCATGTGGGACTGCGATGTATGTGGCGGATGT	CCGAGTG	3071	
Db	3004	ATACCCCTCTTTTGG	CCAGCGTGTGCGCAATCTTGTGGTCTTAACTTTTCTTA	3063		
Qy	3072	ATTCCCTCTCTTGG	CCACCGTGTGATCGGCAATCTTGTGGTCTTAACTTTTCTTA	3131		
Db	3064	GCTTTGGCTTTTGG	CAACTTCGGTTCATCTAGTCTTTATCAGCCCCGACTGCGGACAATGAT	3123		
Qy	3132	GCCTTGCTTTTGT	CAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCGGATAACGAT	3191		
Db	3124	ACGAATAAAAATCG	AGAGGCTTCAATCGTATGTCTGTTTTAAGAACTGGGTGAAACGT	3183		
Qy	3192	ACGAATAAAAATAG	CGAGCGCTTCAATCGAATTTGGCCGATTTAAAGTTTGGGTTAAGCGT	3251		
Db	3184	ANATATCCCGATTG	TTTTTAAGTTTAATTCGAAATAAATTGACAAATCAAAATAGTGACCAA	3243		
Qy	3252	ANATATGCTGATTG	TTTCAAGTTTAATGCTAACAAATGACAAATGACAAATCAAAATAGTGATCAA	3311		
Db	3244	CCATCAG-----A-CA-	-----TGS--CGAT-A--ATG-----	3265		
Qy	3312	CCATCAGGTGAGAGG	CAACACAGATCAGTTGGATTTGGAGCGAGAGCATGGTGACAAC	3371		
Db	3266	-A	CTGAGTTGGTCA	TGACGAAATCATGGCGGATGGCTGTGATCAAAAAGGGTATGAAG	3324	
Qy	3372	GAACTGAGCTGGG	CCACGACGAGATCTCTCGCGACGGCCTCATCAAGAAGGGGATCAAG	3431		
Db	3325	GGCGAGACCAGCTG	GAGGTGGCCATTGGCGATGGATGGAGTTCCACGATACATGCGCAT	3384		
Qy	3432	GAGCAGACGCACT	GAGGTGGCCATCGGGGATCGGATGGAAATTCACGATACACGGCGAC	3491		
Db	3385	ATGAANAACCAAC	AGCCCAAGAAATCAATAATCATGAACAACACACAGCATGATTGGAAC	3444		
Qy	3492	ATGAAGAACAACA	AGCGGAAGAAATCCAATAATCTAAATAACGCAACGATGATTGGCAAC	3551		
Db	3445	TCAATAAACCAACA	GACNAATAGACTTGGAAATGAGCTTAACCCATAGAGGTTTGTCCATA	3504		
Qy	3552	TCAATTAACCAACA	NACNATAGACTTGGAAACGAGCTAAACCATAGAGGTTTGTCCATA	3611		
Db	3505	CAGCAGATGACACTG	CCAGCTTAATCTCATATGTTAGCCATAAGAAATGCAACATTCAG	3564		
Qy	3612	CAGGACGACGACH	CTGCCAGCTTAATCTCATATGTTAGCCATAAGAAATGCAACATTCAG	3671		
Db	3565	GACGAGACCAACA	AGGCGACGCCGAGACCATCTGAGGGCGAGGAGAAACGCGAGCTCAGC	3624		
Qy	3672	GACGAGACCAACA	AGGCGACGCCGAGACCATCTGAGGGCGAGGAGAAACGCGAGCTCAGC	3731		
Db	3625	AAAGAGGACCTCG	GCCTCTGACGAGGAACCTGGACGAGGAGCGCGAGGCGGATGAGGGCCAG	3684		

Db	4765	ATTCCAAGACCAGGTGGCGCCACCAAGCAATAGTATCCGAATAGCTTACAGATAAAAA	4824
Qy	4869	ATTCCAAGACCAGGTGGCGCCACCAAGCAATAGCTTTGAATAGTAAACCGATAGAAA	4928
Db	4825	TTCGATATAATCAATTATGTTGTTCAATGGCTTAAACATGTTTACCATGACCCCTCGATCGG	4884
Qy	4929	TTCGATATAATCAATTATGTTTCAATGGCTGAACATGTTACCAATGACCCCTCGATCGT	4988
Db	4885	TACGAGCCCTCCGAGGCCGTACAACAATGCTCCTCGACAAATCAATGGGATATTCGTAGTT	4944
Qy	4989	TACGATGCGTCCGACACGTTATACCGCGCTCTAGACTATCTCAATGCGATATTCGTAGTT	5048
Db	4945	ATTTTCAGTGGCGAATGCTCTATTAATAATATCCGTTTACGATATCACATTTTCAAGAG	5004
Qy	5049	ATTTTCAGTTCGGAATGCTCTATTAATAATATCCGTTTACGATATCACATTTTATGAG	5108
Db	5005	CCATGGAATTTATTCATGTAGTGTGTCATTTTATCCATCTTAGTCTCTGTACTCACG	5066
Qy	5109	CCATGGATTTATTCATGTAGTGTGTCATTTTATCCATCTTAGTCTCTGTACTCACG	5168
Db	5065	GACATCATTCGAGAAGTATTTTCGTATCGCGGACACTGCTCCGTGTGGTGAGAGTGGCCAAA	5124
Qy	5169	GATATTATCGAGAAGTACTTCGTGTGGCGGACCCCTGCTCCGAGTGGTGGCTGGCGGAAA	5228
Db	5125	GTGGTCTGCTCTCGTGGTTAGTCAAGGTGTCGAAGGTATCCGGACGTTCTGTTTTCGGG	5184
Qy	5229	GTGGGCGGTGCTCTCGATGTTGAAGGAGCCAGGCGCATTCGGACACTGCTCTTCGGG	5288
Db	5185	TTAGCCATGTCTGTGCTGCTTATTCAACATTTGCTGTGTTGTTCTTTGGTGATGTTTC	5244
Qy	5289	TTGGCCATGTGCTGCGCGCCCTGTTCAACATCTGCCCTGCTGTCTCTGTGCTGATGTTTC	5348
Db	5245	ATCTTTGCTATCTTTGGGATGTCCTTCTTCATGCAATGTCAAGAGAGAGCGGCATAAAT	5304
Qy	5349	ATCTTTGCCATTTTCGGCATGTGCTTCTATGTCACGTGAAGGAGAGAGCGGCATTAAAC	5408
Db	5305	GCTGTGTATAATTTAAGACATTTGGCCAAAGATATGATATTCCTGTTTCAGATGTCTTACC	5364
Qy	5409	GACGCTACAACITCAAGACCTTGGCCAGACATGATCCTGCTCTTCAGATGTGCGACG	5468
Db	5365	TCAGCCGTTGGGATGGTGTGTTAGATGCCATTTCAATGAGGAAAGATGGGATCCACCC	5424
Qy	5469	TCAGCCGTTGGGATGGTGTGTTAGTGGACGCATTATCAATGAGGAAAGATGGGATCCACCC	5528
Db	5425	GACACGACAGGGCTATCCGGGCAATTTGGTGTACGAGCTTGTGGAATTAACGTTTCTC	5484
Qy	5529	GACACGACAAAGGCTATCCGGGCAATTTGGTGTACGAGCGGTTGGAAATACGTTTCTC	5588
Db	5485	CTTTCATATCTAGTATAAGCTTTTGTAGATTTTAAATATGATGCTCATTCCTCATTCCTC	5544
Qy	5589	CTTCATACCTAGTATAAGCTTTTGTAGTATTATTAATATGATGCTCATTCCTCATTCCTC	5648
Db	5545	GAGAACTATACCGAGGCTACGAGGATGTACAGGAGGTCCTACCGACGAGATATATGAT	5604
Qy	5649	GAGAACTATAGTCAGGACCCGAGGACGTGCAAGAGGGTCTTAACCGACGAGCATAGCAC	5708
Db	5605	ATGTACTACGAGATTTGGCAACAATTCGATCCGAGGGTACCAGTACATACGATAGCAC	5664
Qy	5709	ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGGGACCCAGTACATACGCTATGAT	5768
Db	5665	CAGCTGTCCGAGTTCCTGGAGCTGTGGAGCCGCGCTCGAGATCCACAGCCGAAACAG	5724
Qy	5769	CAGCTGTCCGAAATTCCTGGACACTGAGAGCCCGCGCTCGAGATCCACAAACCGAAACAG	5828
Db	5725	TACAAAATCATATCGATGGACATGCCGATATGTGGGGGACATGATCTACTGTGTGGAT	5784
Qy	5829	TACAAGATCATATCGATGGACATACCCATCTGTCCGGGTGACTCATGTACTGGGTGCAC	5888
Db	5785	ATATTGGATGCCCTGACCAAGGACTCTTTTCCGCGCAAGGGTAATCCGATCGAGAGACG	5844
Qy	5889	ATCTTCGAGCCCTTACGAAAGACTCTTTTCCGCGAAGGCAATCCGATAGAGAGACG	5948

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Db 5845 GGTGAATGGTGAGATACGGCGCGACCCGACACCGGAGGCTATGATCGGTTGCTGCG 5900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5949 GGTGATGGTGAGATACGGCGCGCGGATACGGAGGCTACGAGCCGCTCATCA 6008
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5905 ACGTGTGGCGCCAGCGTGAGAGTACTGCGCCAGCTGATACAGATGCGGTGCGG 5960
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6009 ACGTGTGGCGTCAAGGTGAGGAGTACTGCGCCGCGCTAACTTACGACGCGCTGCGG 6064

RESULT 11
ID US-08-808-793-26 STANDARD; DNA; UNC; 1237 BP.
AC xxxxxx
DT
CC Sequence 26, Application US/08808793
CC Sequence 26, Application US/08808793
CC GENERAL INFORMATION:
CC APPLICANT: Soderlund, David M.
CC APPLICANT: Ingles, Patricia J.
CC TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC TITLE OF INVENTION: AND USE THEREOF
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC STREET: Clinton Square, P.O. Box 1051
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/808,793
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/034,361
CC FILING DATE: 24-DEC-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/012,649
CC FILING DATE: 01-MAR-1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Braman, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 716-263-1636
CC TELEFAX: 716-263-1600
CC INFORMATION FOR SEQ ID NO: 26:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1237 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC SEQUENCE 1237 BP; 310 A; 309 C; 293 G; 325 T; 0 OTHER.
SQ

Query Match 7.2%; Score 472; DB 21; Length 1237;
Best Local Similarity 76.6%; Pred. No. 0.00e+00;
Matches 679; Conservative 0; Mismatches 207; Indels 0; Gaps

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	Query Match	7.28;	Score 472;	DB 21;	Length 1237;
	Best Local Similarity	76.68;	Pred. No. 0.00e+00;		
	Matches 679;	Conservative	0;	Mismatches 207;	Indels 0;
	Gaps				
Db	187	ACAACTCTCGCTGGGCAATATTTCAAGTCGGTCGACTCAACCACACGACGTTGAGCCA	246		
Qy	4415	ACAGCTTTTTGCTGGAAAATATTTTAAGTCGAGGACATGAATGGCACGAAGCTCAGCCA	447		
Db	247	CGAAATCATCCACACGGGAATCGGTGCATCTTAGAGAACTACACCTGGGAGAACTCACCC	306		
Qy	4475	CGAGTCATACCAAATCGCAATGCTTSCGAGAGCGAGAACTACACGTGGTGAATTCAGC	453		



Db	4792	GTCACTCCTCTCCATTGTGGGAATGTTCTCGCTGATATCATTTGAGAAAGTACTTCGTCTCC	4851
Qy	5136	GTCAATTTTATCCATCTTAGGCTCTGACTTAGCGCATATATTCGAGAAAGTACTTCGTGTGG	5195
Db	4852	CCAAACCTATATCCGAGTTATCCGATGTGGCCGTTATTTGGCGCATCTTCGCTCTGATCAAG	4911
Qy	5196	CCGACCCTGCTCCGAGTGTGCTGTGGCGAAAGTGGCGCGTTCCTTCGACTGTGGGAAG	5255
Db	4912	GGCGCAAAAGGATCGCACCTGCTCTTTGGCTTAATGATGTGCGCTGCGCGCCCTGTGTTG	4971
Qy	5256	GGAGCCAAGGCCATTCGGACATGCTCTTCGCGTTGGCCATGTCGCTGCCGCGCTGTTC	5315
Db	4972	AACATCGGCCCTCTGCTCTTCTCTGCTCAATGTTCACTTCTTCATTTTGGCATGTTCCAA	5031
Qy	5316	AACATCTGCTGCTGTTCTCTGCTCATGTTCACTTTCGTCATTTTTCGGCATGTGGTTC	5375
Db	5032	TTGCATACGTGTGAAGCACGAGCGCGCATTTGACGACATGTTTCAACTTCGAGACATTTGGC	5091
Qy	5376	TTCAATGCACTGTAAGCGAGAGAGCGGCATTAACGACGCTACAACCTCAAGACCTTTGGC	5435
Db	5092	AACAGCAGATCTGTTGTTTTCAGATCAACAGCTGCTGCTGGCTGGGATGGCTGCTGCTG	5151
Qy	5436	CAGACGATGATCTGCTCTTTTCAGATGTGCGAGCTCAGCGGTTGGGATGGGTACTGGAC	5495
Db	5152	CCATCTCTGAACCGCCCTCGTCACTGCAGCTTGGACAAGACGACCCAGGGAGTGGCTTC	5211
Qy	5496	GCCATTAATCAATGNGNAGC--A-TGC-GATCC-ACCC-GR-CAGCGACAAAG--GCTAT	5546
Db	5212	AAAGGGAGCTGTGGGAACCCCTCGGTGGGCATCTTCTCTTTGTGAGCTACATCATCTC	5271
Qy	5547	CCGGGCAATGTGGTTTCAGCGSACCGTTGGAATAAGCTTCTCTCTCATACCTAGTTATA	5606
Db	5272	TCCTTCTCTGATGTGGTGTGAACATGTACATCGGCATCATCTCGGAGAACCTTCAGCGTGGCC	5331
Qy	5607	AGCTTTTGTAGTTATTAATATATGATATGCTGTGCTCATCTCAGAACTATAGTCAGGCC	5666
Db	5332	ACCGAGGAGCGCCGACCTCTGAGTGGAGATGACTTCGAGAGCTTTCTATGACATCTGG	5391
Qy	5667	ACCGAGGACGTGCAAGAGGGTCTCAACCGACGACGACTACGATCTAGTATGAGATCTGG	5726
Db	5392	GAGAAGTTTGACCCAGACGCCACCCAGTTTCATGCGACTACTGTAAAGCTGGCAGACTTTGCC	5451
Qy	5727	CAGCAATTCGATCCGGAGGACCCAGTACATACGCTATGATCAGCTGTCCGAAATTCCTG	5786
Db	5452	GACGCCCTTGGAGCACCGCTCCGAGTACCCCAAGCCCAACCAACCATCGAGCTATGCCCATG	5511
Qy	5787	GACGTACTTGGAGCCCGCTGCGATCTCACAAACCGAAGATACAAGATCATATCGATG	5846
Db	5512	GACCTGCCATCTGTGACGGGAGATCGCATCCATGCTTGGACATCTTTTTCGCTTTCACC	5571
Qy	5847	GACATACCCATCTCTCGGGTGACCTCATGCTACTGCGTCGACATCCTCGACGCCCTTAGC	5906
Db	5572	AA 5573	
Qy	5907	AA 5908	

RESULT	13
ID	US-09-024-020A-2 STANDARD; DNA; UNC; 6007 BP.

AC  
DT  
DE  
CC  
CC

CC APPLICANT: DELGADO, STEPHEN G.  
CC APPLICANT: DIETRICH, PAUL S.  
CC APPLICANT: FISH, LINDA M.  
CC APPLICANT: HERMAN, RONALD C.  
CC APPLICANT: SANGAMESWARAN, LAKSHMI  
CC TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
CC SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
CC NUMBER OF SEQUENCES: 42

CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: JANET PAULINE CLARK  
CC STREET: 3401 HILLVIEW AVENUE, MS A2-250  
CC CITY: PALO ALTO  
CC STATE: CA  
CC COUNTRY: U.S.A.  
CC ZIP: 94304-1397  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: FLOPPY disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/09/024,020A  
CC FILING DATE: 16-FEB-1998  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 60/039,447  
CC FILING DATE: 26-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: CLARK, JANET P.  
CC REGISTRATION NUMBER: 34,799  
CC REFERENCE/DOCKET NUMBER: R0020B-REG  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (650) 852-3097  
CC TELEFAX: (650) 855-5322  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6007 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC SEQUENCE: 6007 bp: 1490 A: 1559 C: 1609 G: 1349 T: 0 OTHER.

Query Match	5.5%	Score 356;	DB 23;	Length 6007;
Best Local Similarity	65.18;	Pred. No. 0.00e+00;		
Matches	899;	Conservative	0;	Mismatches 471; Indels 12; Gaps 9;
Db	4225	ATCAACTTTTGACAATGTGCGAGCAGGCTAGCTGGCCCTTCTTCAAGTGGCACTCTCAAA	4284	
Qy	4536	ATGAATTTTCGATCATGTAGTAAAGCGCTATCTGTGCGCTTTTTCAAAGTGGCAGCTCTCAAA	4595	
Db	4285	GCGTGGATGGACATCATGTATGCGCGCTGTAGATTCGCGAAGCCAGACGAGCAGCGCTGAC	4344	
Qy	4596	GCGTGGATACAAATCATGAACGATGCTATCGATTACAGAGAGTGGACGAACGACACCAATT	4655	
Db	4345	TACGAGGGCAACATCTACATCTACATCTTCGTCTATCTTTCATCATCTTCCTGGCTCCTTC	4404	
Qy	4656	CGTGAACGCAACATCTACATGATTTATTTCTGTTATTTCTTCATCATATTTGGATCCTTT	4715	
Db	4405	TTCAACCTCAACCTGTTTCATGGTGTCAATCATCGACAACCTTCACACGACGACGAGAAAG	4464	
Qy	4716	TTCAACACTCAATCTGTTTCATTTGGTGTATCATTTGATTAATTTTATGACGAAAGAAAAA	4775	
Db	4465	TTTGGAGG--TCAG--GACATCTTCATGACAGAGAAACAGAAAGAGTACTCAATGCGCATG	4521	
Qy	4776	GCAGGTGGATCATTTAGAAATGTTTCATGACAGAGATCAGAAAGTACTATAATGCTATG	4835	
Db	4522	AAAAAGCTGGGTCCCAAGAGCCACAGAAAGCCCATCCCGCCGCTTTGAAACAAATCCAA	4581	
Qy	4836	AAAAAGATGGGCTCTAAAAAACCATTTAAAAGCCATTTCCAAGACCAAGTGGCGACCCAA	4895	
Db	4582	GGGATGCTCTTTGATTTTCGTCACTCAACAGCCCTTTTGACATGTTGATCATGCTCATC	4641	
Qy	4896	GCAATAGTCTTTTGAATAGTATACCGATAGAAATTCGATATAATCATTTATGTTATTCATT	4955	
Db	4642	TGCGTTTAAACATGGTGACAATGATGGTGAGACAGACACTCGACGCAACGATGGAGAAC	4701	
Qy	4956	GGTCTGAACATGTTTACCATGACCCCTCGATCGTTACGATGGCTCGGACACGTAATACGCG	5015	
Db	4702	ATTCTTTTACTGGAAATTAATCTGGCTTTTGTGTCATCTTCTTCAACCTGGGAGTGTGCTCAAA	4761	

QY	5016	GTCTTAGACTATCTCAATCGGATATTCGTAGTATATTTTCAGTTCCGAAATGCTATTAAAA	5075
Db	4762	ATGTTTGCCCTTGAGACACTACTATTATTCACCATTGGCTGGAAACATCTTTTGACTTTGTGGTG	4821
QY	5076	ATATTGCGCTTTACGATATCACTATATTTATGAGCCATGGAATTTATTTGATGTAGTAGTT	5135
Db	4822	GTCACTCCTCTCCATGTGTGGGAATGTTCTCTGGCTGATATCATTTGAGAAGTACTTTGCTGCTCC	4881
QY	5136	GTCAATTTTATCCATCTTAGTGTCTTGTACTTAGCGATATTTATCGAGAAGTACTTTGCTGCTCG	5195
Db	4882	CCAACCTTATTCGGAGTTATCCGATTGGCCCGTATTTGGCGCATCTTTGCGTCTGATCAAG	4941
QY	5196	CCGACCTCTCGAGTGTGTGTGGGAAAGTGGGCCGTCTCTCGACTGGTGAAG	5255
Db	4942	GGCGCCAAAGGATCCGCACCTCGTCTTTGCTCTTAATGATGTGCTGCTGCCGCCCTCTTC	5001
QY	5256	GGAGCCAAAGGATTCGGACACTGCTCTTCGCGTTGGCCATGTGCGTGGCGCCCTGTTCT	5315
Db	5002	AACATCGGCCCTGCTGCTCTTCTCTGTCATGTTTCATCTTCTTCATTTTGGATGTCTCAAC	5061
QY	5316	AACATCTGCTGCTGCTGCTCTGTCATGTTTCATCTTTGCGATTTTCGGCATGTCTGTTCT	5375
Db	5062	TTGCGATACGTGAAGCACGAGCGCGCATTTGACGACATGTTTCAACTTCGAGACATTTGGC	5121
QY	5376	TTCTGCGCGTGAAGGAGAAGAGCGGCATTTAACGACGTCTACAACCTTCAAGACCTTTGGC	5435
Db	5122	AACAGCATGATCTGTTTGTTCAGATCAACAGCTGCTGCTGGGTGGGATGGCGTCTGCTGTG	5181
QY	5436	CAGAGCATGATCCTGCTCTTTTCAGATGTGCGAGTCAGCGGTTGGGATGGTGTACTGGAC	5495
Db	5182	CCAATCCTGAACCGGCCCTTGACTGCACTTGGACAAAGAGCACCCAGGGAGTGGGTTTC	5241
QY	5496	GCCATTATCAATGAGGAAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAAG--GCTAT	5546
Db	5242	AAAGGGAGCTGGGGAACCCCTCGGTGGGCATCTTCTTCTTTGTGAGGTACATCATCATC	5301
QY	5547	CCGGCAATGTGGTTTCACGCGACCTTGGAATTAAGCTTTCTCCTCTCATACCTAGTTATA	5606
Db	5302	TCCTTCTGATTGTGTGAACATGTACATCGGCATCATCTCTGGAGAACTTCAGCGTGCC	5361
QY	5607	AGCTTTTGTATGATTAAATATGATACATGCTGTTCATTCGAGAACTATATGTCAGGCC	5666
Db	5362	ACCGGAGAGCGCCGACCCCTCTGAGTGAGGATGACTTCGAGACTTTTATGATGATCTGG	5421
QY	5667	ACCGGAGCGTGCAGAGGGTCTACCGACGACGACTACGACATGTACTATGAGATCTGG	5726
Db	5422	GAGAAGTTTGCCAGACCGCCACCCAGTTTCATCGAGTACTGTAGCTGGCGAGACTTTGCC	5481
QY	5727	CAGCAATTCGATCCGGAGGGCCACCCAGTACATACGCTATGATCAGCTTCTCGGAATTCCTG	5786
Db	5482	GAGCCCTTGAGCACCCGCTCCGAGTTACCAAGCCCAACACCATCGAGCTCATCGCCATG	5541
QY	5787	GACGTACTGGAGCCCGCTGCAGATCCACAACCCGAACAGTACAGATCATATCGATG	5846
Db	5542	GACCTGCCCATGGTGAAGCGGAGATCGCATCCACTGCTTTGGACATCTCTTTTCCCTTCA	5601
QY	5847	GACATACCCATCTGTGCGGCTGACCTCATGTACTGCGTGCAGATCCCTCGAGCCCTTACG	5906
Db	5602	AA 5603	
QY	5907	AA 5908	

RESULT 14  
ID US-09-024-020A-7 STANDARD; DNA; UNC; 6556 BP.  
AC xxxxxx

Sequence 7, Application US/09024020A  
Sequence 7, Application US/09024020A  
GENERAL INFORMATION:  
APPLICANT: DELGADO, STEPHEN G.  
APPLICANT: DIETRICH, PAUL S.  
APPLICANT: FISH, LINDA M.

CC	APPLICANT:	HERMAN, RONALD C.
CC	APPLICANT:	SANGAMESWARAN, LAKSHMI
CC	TITLE OF INVENTION:	NOVEL CLONED TETRODOXIN-SENSITIVE
CC	TITLE OF INVENTION:	SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC	NUMBER OF SEQUENCES:	42
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	JANET PAULINE CLARK
CC	STREET:	3401 HILLVIEW AVENUE, MS A2-250
CC	CITY:	PALO ALTO
CC	STATE:	CA
CC	COUNTRY:	U.S.A.
CC	ZIP:	94304-1397
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/09/024,020A
CC	FILING DATE:	16-FEB-1998
CC	CLASSIFICATION:	536
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 60/039,447
CC	FILING DATE:	26-FEB-1997
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	CLARK, JANET P.
CC	REGISTRATION NUMBER:	34,799
CC	REFERENCE/DOCKET NUMBER:	R0020B-REG
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(650) 852-3097
CC	TELEFAX:	(650) 855-5322
CC	INFORMATION FOR SEQ ID NO: 7:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	6556 base pairs
CC	TYPE:	nucleic acid
CC	STRANDEDNESS:	single
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	DNA (genomic)
CC	SEQUENCE	6556 BP; 1620 A; 1727 C; 1736 G; 1471 T; 2 OTHER.
Qy	Query Match	5.5%; Score 356; DB 23; Length 6556;
Qy	Best Local Similarity	65.1%; Pred. No. 0.00e+00;
Qy	Matches	899; Conservative 0; Mismatches 471; Indels 12; Gaps 9;
Db	4342 ATCAACCTTGCACATGTCGGAGCAGCGGTACTCTGCCCTCTCTTCAAAGTGCGCAACCTTCAA	4401
Qy	4536 ATGAATTTCGATCATGTAGTAGTACGCGTATCTGTGCGCTTTCCAAGTGGCACCTTCAA	4595
Db	4402 GGCTGGATGGACATCATGTATGCGGCTGTAGATTCGGAAGCCAGACGACGCGCTGAC	4461
Qy	4596 GGCTGGATACAATAATGAACGATGCTATCGATTCAGGAGGGTGGACAAGCAACCAATT	4655
Db	4462 TACAGGGCACATCTACATGTACATCTACTTGTGTCATCTTCATCATCTTCGGCTCGTTC	4521
Qy	4656 CGTGAACAGCAACATCTACATGTATTTATATTTTCGTATCTTCATCATATTATTTGGATCGTTT	4715
Db	4522 TTCAACCCTCAACCTGTTTCATCGGTGTCATCATCGACAACCTTCAACGACGAGAAGAAAAG	4581
Qy	4716 TTCACATCAATCTGTTTCATGTTGTTTATCATTGATTAATTTATGAGCAAAAGAAAAA	4775
Db	4582 TTTGGAGG--TCAG--GACATCTTCATGACAGAGAACAGAGAGTACTACAATGCCATG	4638
Qy	4776 GCAGGTGGATCATTTAGAAATGTTTCATGACAGAGAGATCAGAAAAAGTACTATAATGCTATG	4835
Db	4639 AAAAAGCTGGCTCCAGAGAGCCACAGAACCCATCCCCCGACCCCTTGACACAAATCCAA	4698
Qy	4836 AAAAAGATGGGCTCTAAAAACCATTTAAAGCCATTCCAAGACCAAGGTGGCGACCACAA	4895
Db	4699 GGGATGTCCTTTGATTTCGTCACCTCAACAGCCCTTTGCACATTTGTGATCATGATGCTCATC	4758
Qy	4896 GCAATAGCTTTGAAATAGTACCGATAGAAATTCGATATAATCATTTATTTATTCATTT	4955
Db	4759 TGCCTTAACATGTTGACAATGATGTTGGAGACACACACTCAGACGACGACAGATGGAGAAC	4818



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QY 4956 GGTCTGAACATGTCACCATGACCCCTGATCGTTCAGATCGCTCGACAGCTATACGGCG 5015
Db 4819 ATCTCTTACTGGATTATATCTGGTCTTTGTTCATCTCTTCTACCTCGGAGTGTGCTCAAA 4878
QY 5016 GTCTAGACTATCTCATGCGATATTCGTAGTATTTTCAGTTCCGAACTCTATTAAA 5075
Db 4879 ATGTTGCCCTTGAGACACTACTATTACCATTTGGCTGGGAGAACATCTTTGACTTTGGTG 4938
QY 5076 ATATTCCTTTAGCATATCACTATTATTTAGAGCCATGGAATTTATTTGATGTAGTAGTT 5135
Db 4939 GTATCTCTCTCCATTTGGGAATGTTCTCGCTGATATCATTTGAGAGTACTTCGCTCC 4998
QY 5136 GTCATTTATCCATTTAGTCTGTGTTAGCTTAGCGATATTTATCGAGAAGTACTTCGTGTG 5195
Db 4999 CCAACCCCTATTTCGAGTATTCGATTCGCGCCGATTTGGCGCATCTTCGCTCTGATCAAG 5058
QY 5196 CCGNCCCTGCTCCGAGTGGTGGCTGGCGAAGTGGCGCTGCTTCGACCTGGTGAAG 5255
Db 5059 GGGGCCAAAGGAGTCCGACCCCTGCTTTTGGCTTTAAATGATGCGTGGCGCCGCTGTTTC 5118
QY 5256 GGAGCCAAAGGCAATTCGAGACACTGCTCTTCGCGTTGGCCATGTCGCTGCGCGGCTGTT 5315
Db 5119 AACATCGGCTCTCTGCTCTCTGCTGCTATGTTCTATCTTCTCCATTTTGGCATGTCCAAC 5178
QY 5316 AACATCTGCTGCTGCTGCTCTGCTGCTATGTTCTATCTTTTGGCATGTGCTGTT 5375
Db 5179 TTCGCATACGTGAAGCAGCAGGCGGCGGATTCGACACATGTTCAACTTCGAGACATTTGGC 5238
QY 5376 TTCATGACGTGAAGAGAGAGAGCGGCAATTAACGACGCTACAACTTCAAGACCTTTGGC 5435
Db 5239 AACAGCATGATCTGTTTGTTCAGATCACAACGCTCTGCTGGCTGGGATGCGCTGCTGCTG 5298
QY 5436 CAGAGCATGATCTGCTCTTTTACAGATGTCGACGCTCAGCCGCTGGGATGCTGACTGGAC 5495
Db 5299 CCAATCTGAACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5358
QY 5496 GCCATTATCAATGAGGAAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT 5546
Db 5359 AAGGGGACTGTGGGAACCCCTCGCTGGGATCTCTTCTTGTGAGCTACATCATCATC 5418
QY 5547 CCGGGCAATTTGGTTTTCAGCGACCGTTGGATACGTTTCTCTCTCATACCTAGTATA 5606
Db 5419 TCCTTCTGATTTGGTGAACATGATACATCGCCATCATCTCGGAGAACTTCAGCGTGGCC 5478
QY 5607 AGCTTTTGTAGTATTATTAATATGATATGCTGCTCATCTCTCGAGAACTATAGTCAGGCC 5666
Db 5479 ACCGAGGAGCGCCGACCCCTCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGG 5538
QY 5667 ACCGAGGAGCTGCAAGAGGGTCTAACCGACGACCTACGACATGTACTATGAGATCTGG 5726
Db 5539 GAGAAGTTTGACCCAGACGCGCCACCCAGTTTCATCGAGTACTGTAACTGGGACACTTTTGGC 5598
QY 5727 CAGCAATTCGATCCGGAGGACCCAGTACATAGCTATGATGAGCTGTCCGATTCCTG 5786
Db 5599 GACGCCCTGGAGCACCGCTCCGAGTACCCAGCCCAACACCATTCGAGCTCATCGCCATG 5658
QY 5787 GACGTACTGGAGCCCGCTGCAGATCCACAAACCGAAGTACAAGATCATATCGATG 5846
Db 5659 GACCTGCCATGTTGAGGGAGATCGCATCCACCTGCTTGGNACCTCTTTTCGCCCTTCAAC 5718
QY 5847 GACATACCCATCTGCGGGTGAGCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5906
Db 5719 AA 5720
QY 5907 AA 5908
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RESULT 15  
ID US-09-024-020A-8 STANDARD; DNA; UNC; 6826 BP.  
AC xxxxx  
DT  
Db Sequence 8, Application US/09024020A

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CC Sequence 8, Application US/09024020A
CC GENERAL INFORMATION:
CC APPLICANT: DELGADO, STEPHEN G.
CC APPLICANT: DIETRICH, PAUL S.
CC APPLICANT: FISH, LINDA M.
CC APPLICANT: HERMAN, RONALD C.
CC APPLICANT: SANGAMESWARAN, LAKSHMI
CC TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
CC TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC NUMBER OF SEQUENCES: 42
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: JANET PAULINE CLARK
CC STREET: 3401 HILLVIEW AVENUE, MS A2-250
CC CITY: PALO ALTO
CC STATE: CA
CC COUNTRY: U.S.A.
CC ZIP: 94304-1397
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/024,020A
CC FILING DATE: 16-FEB-1998
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 60/039,447
CC FILING DATE: 26-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CLARK, JANET P.
CC REGISTRATION NUMBER: 34,799
CC REFERENCE/DOCKET NUMBER: R0020B-REG
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (650) 852-3097
CC TELEFAX: (650) 855-5322
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6826 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 6826 BP; 1726 A; 1764 C; 1780 G; 1554 T; 2 OTHER.
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Query Match 5.4%; Score 354; DB 23; Length 6826;
Best Local Similarity 65.0%; Pred. No. 0.00e+00;
Matches 898; Conservative 0; Mismatches 472; Indels 12; Gaps 9;

Db 4168 ATCAACTTTGACAATGTCGGAGCAGGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAA 4227
QY 4536 ATGAATTTGATCATGTAGGTAACGCGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAA 4595
Db 4228 GCGTGGATGGACATCATGTATGCGCTGTAGATTCCCGAAAGCCAGACGAGCGCTGAC 4287
QY 4596 GCGTGGATCAATCATGAACGATGCTATCGATTCAGAGAGGTGGCAAGCAACCAAT 4655
Db 4288 TAGAGGGCAACATCATACATCTACTTCGTCTCATCTTTCATCATCTTCGCTCTTTC 4347
QY 4656 CGTGAACGACATCATACATGATTTATTTTCGATTTCTTCATCATATTTGATGCTTT 4715
Db 4348 TTCACCTTCAACCTGTTTCATCGGTGTCATCATCGCACTTCACACGAGCAAGAAAAAG 4407
QY 4716 TTCACACTCAATCTGTTTCATCTGTTGTTATCATTTGATTAATTTAATGAGCAAAAAA 4775
Db 4408 TTGAGAGG-TCAG--GACATCTTCATGACAGAGGACACAGAAAGTACTATATGCTCAT 4464
QY 4776 GCAGGTGGATCATTAAGAAATGTTTCATGACAGAGATCAGAAAAAGTACTATATGCTAT 4835
Db 4465 AAAAAGCTGGGTCTCCAAAGAGCCACAGAGCCCATCCCCCGACCTTTGAACAAAAATCCA 4524
QY 4836 AAAAAGATGGCTCTAAAAAACCAATTAAAAAGCCATTCCCAAGACCAAGGTGGGAGCCACA 4895
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Search completed: Wed Jul 8 04:28:31 1998  
Job time : 9438 secs.

D	b	4525	GGGATGTCCTTTGATTTCTGCTACTCAACAAGCCCTTTGACATGTGTGATCATGANGCTCATC	4584
Q	y	4896	GCAATAGTCTTTGAAATAGTAAACCGATAGAATAATCGATATAAATCAATTATGTTATTCAAT	4955
		4585	TGCCTTAACATGCTGACAAATGATGTTGGAGACAGACACTCAGACCAAGCAGATGGAGAAC	4644
Q	y	4956	GGTCTGAACATGTTCCACATGACCCCTCGATCGTTACGATGCGTCGGACACGATATAACGCG	5015
		4645	ATTCTTTACTGGAAATTAATCTGCTCTTTGTCATCTTCTTCACTCGCTGAGTGTGCTCAAA	4704
Q	y	5016	GTCTAGACTATCTCAATCCGATATTCGTAGTATTTTTCAGTTCGGAATGTCATATTAATA	5075
		4705	ATGTTTGCCCTTGAGACACTACTACTTCAACCAATTTGCTGGAACTCTTTTGACTTTTGCGTG	4764
Q	y	5076	ATATTGCGCTTTACGATATCACATATTATTATTAGCCATGGAATTTATTGATGTAGTAGTT	5135
		4765	GTCACTCTCCATTTGTTGGGAATGTTCTTGCGCTGATATCATTTGAGAGTACTTCGCTCC	4824
Q	y	5136	GTCAATTTATCCATCTTAGGCTCTGTACTTAGCGATATATTCGAGAAGTACTTCGCTCG	5195
		4825	CCAACCCATTTCGAGTTATTCGGATTGGCCCGTATTGGCGCATCTTTCGCTCATCAAG	4884
Q	y	5196	CCGACCTGCTCCGAGTGTGGTGGGAAATGGCCGTGCTCTTCGACTGGTGAAG	5255
		4885	GGCCGCCAAAGGATCCGCACCTCTGCTTTGCTGTGATGATGTGCTGCTGCCGCCCTGTC	4944
Q	y	5256	GGAGCAAGGCATTCGGACACTGCTCTTCGGGTTGGCCATGTCGCTGCGGCCCTGTC	5315
		4945	AACATCGGCTCTGCTCTCTCTCTGTCATGTTTCATCTTCTCATTTTGGATGCTCCAC	5004
Q	y	5316	AACATCTGCCCTGCTGTTCTCTGCTCATGTTTCATCTTTTGGCATTTTCGGCATGCTGCTTC	5375
		5005	TTCCGATACGTGAAGCACGAGCCGACATGACACATGTTCAACTTCGAGACATTTGGC	5064
Q	y	5376	TTCATGCAGCTGAAGGAGAGAGCGGCATTACGACGCTACAACCTCAAGACCTTTGGC	5435
		5065	AACAGCATGATCTGTTGTTTCCAGATCAACAGCTGCTGCTGGCTGGATGGCTGCTGCTG	5124
Q	y	5436	CAGAGCATGATCTGCTCTTTTCAGATGTCGAGCTCAGCCGTTGGATGGTGTACTGGAC	5495
		5125	CCAACTCTGAACCCGCCCTGACTGCGAGTGTGGACAAAGAGCACCCAGGGAGTGGCTTC	5184
Q	y	5496	GCCATTATCAATGAGGAAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT	5546
		5185	AAGGGGACTGTGGGAACCCCTCGGTGGCATCTTCTTTGTGAGCTACATCATCATC	5244
Q	y	5547	CCGGGCAATTTGTTGTTACGCGACCGTTGGAATTAACGTTTCTCCCTCATACCTAGTTATA	5606
		5245	TCCTTCTGATTTGTTGAACTATGTCATCGGCATCTCTGGAGAACTTCAGCGTGGCC	5304
Q	y	5607	AGCTTTTGATAGTTATTATATGATACATTTGCTGTCATCTCGAGACTATAGTCAGGCC	5666
		5305	ACCGAGAGAGCCGACCCCTCTGAGTGAAGATGACTTCGAGACTTTCTATGAGATCTGG	5364
Q	y	5667	ACCGAGGACGTGCAAGAGGGTCTAACCGACGACGACTACGACATGTACTATGAGATCTGG	5726
		5365	GAGAAGTTTGACCCACACGCCACCCAGTTCATCTGAGTACTGTAGCTGGCAGACTTTGCC	5424
Q	y	5727	CAGCAATTCGATCCGGAGGCCACCCAGTACATACGCTATGATCTAGCTGTCCGAAATCCTG	5786
		5425	GAGCCCTTGAGCACCCGCTCCGAGTGACCCAGCCCAACACCATCGAGCTCATGCCCATG	5484
Q	y	5787	GAGTACTGGAGCCCCGCTGCAGATCCACAACCGAACACAGTACAGATCATATCGATG	5846
		5485	GACCTGCCCATGTTGAGCGGAGATCGCATCCACTGCTTTGGACATCTTTTTCGCTTCACC	5544
Q	y	5847	GACATACCCATCTGTGCGGTGACCTCATGTACTGCTCGACATCTCTCGAGCCCTTACG	5906
		5545	AA 5546	
Q	y	5907	AA 5908	

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W P S R L H (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 7 18:44:09 1998; MasPar time 7952.09 Seconds  
1366.703 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-554-424-7  
Description: (1-6513) from US08554424.seq  
Perfect Score: 6513 1 TCTAGAGCTTGGCCGATAG.....ACCGAGTATTAGCTCTAGA 6513  
N.A. Sequence: AGATCTGCAACCGCGTATC.....TGGCGCTAATCGAGATCT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 457396 seqs, 834342348 bases x 2

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: emb154

Database: genbank106  
1:em\_ba 2:em\_htg 3:em\_hum1 4:em\_hum2 5:em\_in 6:em\_om  
7:em\_or 8:em\_ov 9:em\_pat 10:em\_pl 11:em\_ro 12:em\_v1  
13:gb\_ba 14:gb\_htg 15:gb\_in 16:gb\_om 17:gb\_ov 18:gb\_pat  
19:gb\_ph 20:gb\_pl 21:gb\_pr1 22:gb\_pr2 23:gb\_ro 24:gb\_st  
25:gb\_sy 26:gb\_un 27:gb\_v1

Statistics: Mean 12.782; Variance 6.793; scale 1.882

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6513	100.0	6513	18	Sequence 7 from patent	0.00e+00
2	6513	100.0	6513	18	Sequence 7 from patent	0.00e+00
3	6513	100.0	6513	18	Sequence 7 from patent	0.00e+00
4	5992	92.0	6883	15	Drosophila melanogaster	0.00e+00
5	3676	56.4	6318	15	Musca domestica insect	0.00e+00
6	3676	56.4	6318	15	M. domestica mRNA for v	0.00e+00
7	3664	56.3	6315	15	M. domestica insect	0.00e+00
8	1912	29.4	6096	15	Blattella germanica pa	0.00e+00
9	1910	29.3	6096	15	Blattella germanica pa	0.00e+00
10	1592	24.4	2144	15	Drosophila virilis sod	0.00e+00
11	1441	22.1	5068	15	Blattella germanica pa	0.00e+00
12	696	10.7	986	15	Haematobia irritans pa	0.00e+00
13	694	10.7	986	15	Haematobia irritans pa	0.00e+00
14	485	7.4	1840	15	Drosophila melanogaster	0.00e+00
15	448	6.9	947	15	Haematobia irritans pa	0.00e+00

16	446	6.8	947	15	U83873	Haematobia irritans pa	0.00e+00
17	391	6.0	5616	15	SODNACH	Mus musculus channel m	1.15e-270
18	372	5.7	5352	23	MMU26707	Mus musculus voltage-g	1.23e-255
19	363	5.6	6822	23	RNSCIII	Rat mRNA for brain sod	1.58e-248
20	354	5.4	6826	23	RATSCP6A	Rattus norvegicus sodi	2.00e-241
21	352	5.4	7545	23	RATSCAL	Rat cardiac specific s	7.57e-240
22	342	5.3	6328	21	HUMHBAX	Human voltage-gated so	5.79e-232
23	341	5.2	5203	17	FRBSCAS2	Fugu rubripes mRNA for	3.55e-231
24	341	5.2	7823	21	HUMSKMLA	Homo sapiens skeletal	3.55e-231
25	336	5.2	8552	23	RATNACHI	Rattus norvegicus sodi	3.08e-227
26	336	5.2	8553	23	RNSCPIIR	Rat brain mRNA for sod	3.08e-227
27	334	5.1	6957	23	RATNCHVS	Rat skeletal muscle vo	1.16e-225
28	316	4.9	5952	23	RNU79568	Rattus norvegicus volt	1.66e-211
29	316	4.9	6396	15	ACU66915	Aplysia californica so	1.66e-211
30	320	4.9	8398	23	RNSCPIR	Rat brain mRNA for sod	1.19e-214
31	320	4.9	8399	23	RATNACHI	Rattus norvegicus sodi	1.19e-214
32	320	4.9	8491	21	HUMHHLA	Human cardiac tetradot	1.19e-214
33	316	4.8	9316	23	AF000368	Rattus norvegicus volt	1.66e-211
34	313	4.8	3312	15	DMU26714	Drosophila melanogaste	3.76e-209
35	312	4.8	5955	16	OCU35238	Oryctolagus cuniculus	2.29e-208
36	306	4.7	5505	16	ECU25990	Equus caballus skeleta	1.17e-203
37	308	4.7	6371	21	HSVASCAS	H. sapiens mRNA for vol	3.16e-205
38	302	4.6	542	15	HIU32390	Haematobia irritans ex	1.61e-200
39	298	4.6	6344	23	RNU53833	Rattus norvegicus sodi	2.20e-197
40	296	4.5	6524	23	RNSNS	R. norvegicus mRNA for	8.11e-196
41	296	4.5	6527	9	A58853	Sequence 1 from Patent	8.11e-196
42	296	4.5	6527	9	A58853	Sequence 7 from Patent	8.11e-196
43	296	4.5	7052	9	A58857	Sequence 5 from Patent	8.11e-196
44	284	4.4	6373	23	MMSNS	M. musculus mRNA for SN	2.00e-186
45	279	4.3	4169	15	DMU26716	Drosophila melanogaste	1.62e-182

ALIGNMENTS

RESULT	1	174672	6513 bp	DNA	PAT	23-DEC-1997
LOCUS						
DEFINITION		Sequence 7 from patent US 5688917.				
ACCESSION		174672				
NID		93010813				
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		1 (bases 1 to 6513)				
AUTHORS		Arena, J.P., Feng, G., Hall, L.M., Liu, K., Van Der Ploeg, L.H.T., Wang, P. and Warkme, J.W.				
TITLE		Process for functional expression of the para cation channel				
JOURNAL		Patent: US 5688917-A 7 18-NOV-1997;				
FEATURES		Location/Qualifiers				
source		1. .6513				
BASE COUNT		1681 a 1548 c 1702 g 1582 t				
ORIGIN						

Query Match 100.0%; Score 6513; DB 18; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	TCTAGAGCTTGGCCGATAGACAAATGACAGAAATCCGACTCGATATCTGAGGAAGAAC	60
QY	1	TCTAGAGCTTGGCCGATAGACAAATGACAGAAATCCGACTCGATATCTGAGGAAGAAC	60
Db	61	GCAGTTGTTCCTCCCTTTACCGCGGAATCATTTGGTGAATCGAAACGAGATTCGGC	120
QY	61	GCAGTTGTTCCTCCCTTTACCGCGGAATCATTTGGTGAATCGAAACGAGATTCGGC	120
Db	121	CTGAACATGAAAG	180
QY	121	CTGAACATGAAAG	180
Db	181	ATGGTCCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGGTC	240
QY	181	ATGGTCCGCAAGAAAACAAAAGAAATCCGATATGATGACGAGGAGGATGAAGGTC	240

EXACT MATCH

Db	241	CACAACCGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTTCAGGGCAGCT	300
Qy	241	CACAACCGGATCCCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTTCAGGGCAGCT	300
Db	301	TCCGCGCGGAATGGCTCCACTCCTCTCGAGAGATATCGATCCCTACTACAGCAATGTAC	360
Qy	301	TCCGCGCGGAATGGCTCCACTCCTCTCGAGAGATATCGATCCCTACTACAGCAATGTAC	360
Db	361	TGACATTCGTAGTTGTAGCAAAAGGAAAGATATTTTCGCTTTCTGCAATCAAAGCAA	420
Qy	361	TGACATTCGTAGTTGTAGCAAAAGGAAAGATATTTTCGCTTTCTGCAATCAAAGCAA	420
Db	421	TGTGGATCTCGATCCATTCGAATCCGATACGTCGTGTGGCCATTTACATCTTCTAGTGCATC	480
Qy	421	TGTGGATCTCGATCCATTCGAATCCGATACGTCGTGTGGCCATTTACATCTTCTAGTGCATC	480
Db	481	CATTATTTTCCCTATTCATCATCAGCACAATTCCTGTCACACTGATCCTGATGATATGC	540
Qy	481	CATTATTTTCCCTATTCATCATCAGCACAATTCCTGTCACACTGATCCTGATGATATGC	540
Db	541	CGACAACCCACAGGTTTCAGTCCACTGAGGTGATATTACACGGGAATCTACACATTTCAAT	600
Qy	541	CGACAACCCACAGGTTTCAGTCCACTGAGGTGATATTACACGGGAATCTACACATTTCAAT	600
Db	601	CAGCTGTTAAAGTGTAGTGCAGAGGTTTCATTTTATGCCCCGTTTACGTATCTTAGAGATG	660
Qy	601	CAGCTGTTAAAGTGTAGTGCAGAGGTTTCATTTTATGCCCCGTTTACGTATCTTAGAGATG	660
Db	661	CATGGAATTTGGTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT	720
Qy	661	CATGGAATTTGGTGGACTTCGTAGTAATAGCTTTAGCTTTATGTGACCATGGGTATAGATT	720
Db	721	TAGTAAATCTAGCACCCCTGCGAAGCTTTAGGTGCTCGAGAGCGTTAAACCCGTAGCCA	780
Qy	721	TAGTAAATCTAGCACCCCTGCGAAGCTTTAGGTGCTCGAGAGCGTTAAACCCGTAGCCA	780
Db	781	TTGTGCCAGGCTTGAAGACCATCGTCGCGCGCGTCAATCGAATCGGTGAAGAATCTGCGCG	840
Qy	781	TTGTGCCAGGCTTGAAGACCATCGTCGCGCGCGTCAATCGAATCGGTGAAGAATCTGCGCG	840
Db	841	ATGTGATTAATCTGACCATGTTCTCCCTGTCGGTGTTCGGTTCGATGGCCCTACAGATCT	900
Qy	841	ATGTGATTAATCTGACCATGTTCTCCCTGTCGGTGTTCGGTTCGATGGCCCTACAGATCT	900
Db	901	ATATGGCGTGCTACCGAGAGTGCATCAAGAAAGTTCCCGTGGACGCGTTCCTGGGSCA	960
Qy	901	ATATGGCGTGCTACCGAGAGTGCATCAAGAAAGTTCCCGTGGACGCGTTCCTGGGSCA	960
Db	961	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCCAATTTGGTATTCGGAGG	1020
Qy	961	ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCCAATTTGGTATTCGGAGG	1020
Db	1021	ACGAGGGCATCTCATTTCGGTTATGGGCAATATATCCGGTGGGGCAATCCGACGACG	1080
Qy	1021	ACGAGGGCATCTCATTTCGGTTATGGGCAATATATCCGGTGGGGCAATCCGACGACG	1080
Db	1081	ATTACGTGTGCTCGAGGGGTTTGGTCCGAATCCGAATATGGCTACACAGCTTCGATT	1140
Qy	1081	ATTACGTGTGCTCGAGGGGTTTGGTCCGAATCCGAATATGGCTACACAGCTTCGATT	1140
Db	1141	CGTTCGGATGGGCTTTCCTGTCCGCTTCGAGTATGACACAGGACTTCTGGGAGGATC	1200
Qy	1141	CGTTCGGATGGGCTTTCCTGTCCGCTTCGAGTATGACACAGGACTTCTGGGAGGATC	1200
Db	1201	TGTACAGCTGTGTGTGCGCGCGCGGACCATGGCAGATGCTGTTCTTATAGTCAATCA	1260
Qy	1201	TGTACAGCTGTGTGTGCGCGCGCGGACCATGGCAGATGCTGTTCTTATAGTCAATCA	1260
Db	1261	TCTTCCTAGCTTCATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATCTCGTATG	1320
Qy	1261	TCTTCCTAGCTTCATCTATCTTGTGAATTTGATTTTGGCCATTTGTCATCTCGTATG	1320
Db	1321	ACGAATTCGAAGGAAGGCCGGAAGAGAGGCTGCCGAAGAGAGGCGGATACGTGAAG	1380
Qy	1321	ACGAATTCGAAGGAAGGCCGGAAGAGAGGCTGCCGAAGAGAGGCGGATACGTGAAG	1380
Db	1381	CGGAAGAAGCTCCCGCGCAAGCGGCAAGCTGAGAGAGCGGCCCAATGCGCAGGCTC	1440
Qy	1381	CGGAAGAAGCTCCCGCGCAAGCGGCAAGCTGAGAGAGCGGCCCAATGCGCAGGCTC	1440
Db	1441	AGGACAGCAGCGGATCGGCTGCCGCCGAAGAGGCTGCATGCAATCCGGAATGGCCAAGA	1500
Qy	1441	AGGACAGCAGCGGATCGGCTGCCGCCGAAGAGGCTGCATGCAATCCGGAATGGCCAAGA	1500
Db	1501	GTCGCGAGCTATTCTTGCAATCAGCTATGAGCTATTGTTGGCGCGGAGAGGCAACGATG	1560
Qy	1501	GTCGCGAGCTATTCTTGCAATCAGCTATGAGCTATTGTTGGCGCGGAGAGGCAACGATG	1560
Db	1561	ACAACAACAAGAGAAGATGTCCATTCCGAGCGTGGAGTGGAGTCCGAGTCCGAGCG	1620
Qy	1561	ACAACAACAAGAGAAGATGTCCATTCCGAGCGTGGAGTGGAGTCCGAGTCCGAGCG	1620
Db	1621	TTATACAAAGACAACAGCACCTACACAGCACCAAGCTACCAAAAGTTCGTAAGTGA	1680
Qy	1621	TTATACAAAGACAACAGCACCTACACAGCACCAAGCTACCAAAAGTTCGTAAGTGA	1680
Db	1681	GCAGCATCTCTTATCTTACCTTACCTGTTTACCGCTTTAAACATACGAGGGGATCACGTAGTT	1740
Qy	1681	GCAGCATCTCTTATCTTACCTTACCTGTTTACCGCTTTAAACATACGAGGGGATCACGTAGTT	1740
Db	1741	CTCACAAGTACAGATACGGAACGAGCGTGGCGCTTTGGTATACCCGGTAGCGATCGTA	1800
Qy	1741	CTCACAAGTACAGATACGGAACGAGCGTGGCGCTTTGGTATACCCGGTAGCGATCGTA	1800
Db	1801	AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCACTTGCCCTATGCCGAGCT	1860
Qy	1801	AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCACTTGCCCTATGCCGAGCT	1860
Db	1861	CGAATGCCGTCAACCGATGTCGGAAGAGAAATGGGCGCATCATAGTGGCCGTGACTATG	1920
Qy	1861	CGAATGCCGTCAACCGATGTCGGAAGAGAAATGGGCGCATCATAGTGGCCGTGACTATG	1920
Db	1921	GCAATCTAGGCTCCCGACACTCATCTGATACCTCGCATCAGTCCCGCAATATCGTATACCT	1980
Qy	1921	GCAATCTAGGCTCCCGACACTCATCTGATACCTCGCATCAGTCCCGCAATATCGTATACCT	1980
Db	1981	CACATGCGGATCTACTCGGGCGCATGCGCGTCAATGCGGCTCAGCACAAATGACCAAGGAGA	2040
Qy	1981	CACATGCGGATCTACTCGGGCGCATGCGCGTCAATGCGGCTCAGCACAAATGACCAAGGAGA	2040
Db	2041	GCAAAATGCGCAACCGCAACACAGCAATCAATCAGTGGCGCGCACCAATGGCGGCAACA	2100
Qy	2041	GCAAAATGCGCAACCGCAACACAGCAATCAATCAGTGGCGCGCACCAATGGCGGCAACA	2100
Db	2101	CCTGCTGACACCAATACAAAGCTCGATCATCGGACTACGAAATTTGGCTTGGAGTGA	2160
Qy	2101	CCTGCTGACACCAATACAAAGCTCGATCATCGGACTACGAAATTTGGCTTGGAGTGA	2160
Db	2161	CGGACGAAGCTGGAAGATTAAACATCATGACAATCTTTTATCGAGCCCGTCCAGACAC	2220
Qy	2161	CGGACGAAGCTGGAAGATTAAACATCATGACAATCTTTTATCGAGCCCGTCCAGACAC	2220
Db	2221	AAACGGTGTGATATGAAGATGTGATGCTGCTGATGATGATGATGATGATGATGATGATG	2280
Qy	2221	AAACGGTGTGATATGAAGATGTGATGCTGCTGATGATGATGATGATGATGATGATGATG	2280
Db	2281	GTCGGCACAGTTCGGGCAAGGATCGCGGTGTCTCCGTTTACTATTTTCCCAACAGAGACG	2340
Qy	2281	GTCGGCACAGTTCGGGCAAGGATCGCGGTGTCTCCGTTTACTATTTTCCCAACAGAGACG	2340
Db	2341	ATGACGAGGATGGGCGGACGTTCAAGACAAAGGACTCGAAGTGAATCCTCAAAGGATCG	2400
Qy	2341	ATGACGAGGATGGGCGGACGTTCAAGACAAAGGACTCGAAGTGAATCCTCAAAGGATCG	2400
Db	2401	ATGTGTTTTGTGTGTGGGACTGTTGTGCTGGTGTGTTGTTGAAATTTTCAGGAGTGGGTATCG	2460

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Db 2461 TCATCGCTTCGATCCCTTCGTGAGCTTTCATCAGCTGTGCTATGTGGTCAACACGA 2520  
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Db 2581 GCAACTATTTCTTCACGCCACCTTTCCCATCGAGGCTCCAGGCTCAAGCTATATGSCCATGA 2640  
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Db 2641 GCCCAAGTACTATTTCCAGAGGGCTTGAACATCTTCGACTTCATTTATCGTGGCCCTAT 2700  
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QY 2701 CGCTATTTGGAACGGGACTCGAGGGTGTCCAGGGTGTCCGGTATTCGGTTCCTTTTCGAT 2760  
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Db 2761 TGTGCGCTGTATTCAAACTGSCCAAGTCTTGGCCACACTTAATTTACTCATTTTCGATTA 2820  
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Db 2821 TGGGACACCATGGGCGCTTGGGTAATCTGACATTTGTACTTTGCATTTATCATCTTCA 2880  
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QY 2821 TGGGACACCATGGGCGCTTGGGTAATCTGACATTTGTACTTTGCATTTATCATCTTCA 2880  
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Db 2881 TCCTTGGGGTATGGGAATGCAACTGTTCGGAAAGAAATATCATGATCAACAAGACCGCT 2940  
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QY 2881 TCCTTGGGGTATGGGAATGCAACTGTTCGGAAAGAAATATCATGATCAACAAGACCGCT 2940  
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QY 2941 TTCCGGATGGGACCTCCGCGCTGGGAATTCACCGACTTTATGCACAGCTTCATGATCG 3000  
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QY 3001 TGTTCGGGTGCTCGGGAGATGGATCGAGTCCATGTGGGACTGATGATGGGCG 3060  
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QY 3421 AGGGGATCAAGGACGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3480  
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Db 3481 TACAGGGGACATGAAGAACACAAAGCGGAGAAATCTCAAAATATCTAAATAACCGCAACGA 3540  
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QY 3481 TACACGGCGNATGAAGAACACAAAGCCGAGAAATCCAAATATCTAAATAACCGCAACGA 3540  
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QY 3541 TGATTGGCACTCAATTAACCAAGACAAATAGACTGGAACACGAGCTAAACCATAGAG 3600  
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Db 3601 GTTTGTCTTACAGGACGAGACACTGCCAGCATTAACATCATATGTTAGCCATAAGAAATC 3660  
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QY 3601 GTTTGTCTTACAGGACGAGACACTGCCAGCATTAACATCATATGTTAGCCATAAGAAATC 3660  
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Db 3661 GACCATTTAAGGACGAGAGCCAAAGGCGAGCCGAGACGATGGAGGGGAGGAGGAAGC 3720  
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QY 4081 TGGACAGAATATTTACGGTTATATCTCTTGGAATATGTTAAATCAAGTGGTGGCGCTCG 4140  
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Db 4501 GCGAGAGCGAGAATACACGCTGGGTGAATTCAGCAATGAATTTTCGATCATGTAGTAAACG 4560  
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QY 4501 GCGAGAGCGAGAATACACGCTGGGTGAATTCAGCAATGAATTTTCGATCATGTAGTAAACG 4560  
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Db 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG 4620  
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QY 4561 CGTATCTGTGCTTTTCCAAAGTGGCCACCTTCAAGGCTGGATACAAATCATGAACGATG 4620  
|||||





BASE COUNT		1681 a	1548 c	1702 g	1582 t	/organism="unknown"	
ORIGIN							
Query Match		100.0%; Score 6513; DB 18; Length 6513;					
Best Local Similarity		100.0%; Pred. No. 0.00e+00;					
Matches		6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Db	1	TC	TAGAGCTTGGCGGCATAGACAAATGACAGAAATTCGGACTCGATATCTCGAGGAAGAC	60			
QY	1	TC	TAGAGCTTGGCGGCATAGACAAATGACAGAAATTCGGACTCGATATCTCGAGGAAGAC	60			
Db	61	GC	AGTTGTTTCCGTCCTTTACCCGCGGAATCATTTGGTGAATTCGACAAACGCGATTGCCG	120			
QY	61	GC	AGTTGTTTCCGTCCTTTACCCGCGGAATCATTTGGTGAATTCGACAAACGCGATTGCCG	120			
Db	121	CT	GAACATGAAAAGCAGAGAGGTGGAAGAAAGAGAGCGGAGGAGGTGCCGCGAT	180			
QY	121	CT	GAACATGAAAAGCAGAGAGGTGGAAGAAAGAGAGCGGAGGAGGTGCCGCGAT	180			
Db	181	AT	GTCTCCAAAGAAAACAAAAGAAATCCGATGATGACGAGGAGGATCAAGGTC	240			
QY	181	AT	GTCTCCAAAGAAAACAAAAGAAATCCGATGATGACGAGGAGGATCAAGGTC	240			
Db	241	CACA	CCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTGCAGGGCAGCT	300			
QY	241	CACA	CCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTTCGATTGCAGGGCAGCT	300			
Db	301	TCCG	CCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360			
QY	301	TCCG	CCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC	360			
Db	361	TG	CATTTCGTAGTTGAAGCAAGGAAAGATATTTTTCGCTTTTCGCATCAAAAGCAA	420			
QY	361	TG	CATTTCGTAGTTGAAGCAAGGAAAGATATTTTTCGCTTTTCGCATCAAAAGCAA	420			
Db	421	TGTG	ATGCTCGATCCATCAATCCGATAGTCGTGTGGCCATTTACATCTAGTGCATC	480			
QY	421	TGTG	ATGCTCGATCCATCAATCCGATAGTCGTGTGGCCATTTACATCTAGTGCATC	480			
Db	481	CATT	ATTTTCCCCTATTCATCATCACCAATCTCTGTCAACTGCATCCTGATGATAATGC	540			
QY	481	CATT	ATTTTCCCCTATTCATCATCACCAATCTCTGTCAACTGCATCCTGATGATAATGC	540			
Db	541	CG	ACAACGCCCGGTTGAGTCCACTGAGTGATATTCACCGGAATCTACATTTGAAT	600			
QY	541	CG	ACAACGCCCGGTTGAGTCCACTGAGTGATATTCACCGGAATCTACATTTGAAT	600			
Db	601	CAG	CTGTTAAAGTGATGCGACGAGGTTTCATTTATGCCGTTTACGTATCTTAGAGATG	660			
QY	601	CAG	CTGTTAAAGTGATGCGACGAGGTTTCATTTATGCCGTTTACGTATCTTAGAGATG	660			
Db	661	CAT	GGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTACCATGGGTATAGATT	720			
QY	661	CAT	GGAATTTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTACCATGGGTATAGATT	720			
Db	721	TAG	TAATCTAGCAGCCCTGCGAACGTTTAGGGTGTGCGAGCGCTTAAACCGTAGCCA	780			
QY	721	TAG	TAATCTAGCAGCCCTGCGAACGTTTAGGGTGTGCGAGCGCTTAAACCGTAGCCA	780			
Db	781	TT	TGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAAGAAATCTGCGG	840			
QY	781	TT	TGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAAGAAATCTGCGG	840			
Db	841	AT	GTGATTTACCTGACCATGTTCTCCCTGTGCGGTGTTGATGGGCTACAGATCT	900			
QY	841	AT	GTGATTTACCTGACCATGTTCTCCCTGTGCGGTGTTGATGGGCTACAGATCT	900			
Db	901	AT	ATGGCGGTGCTACCGAGAAGTGATCAAGAAGTTCCCGCTGGACGGTTCCTGGGGCA	960			
QY	901	AT	ATATGGCGGTGCTACCGAGAAGTGATCAAGAAGTTCCCGCTGGACGGTTCCTGGGGCA	960			
Db	961	AT	CTGACCCGAGGAACCTGGGACTATCACAAATCGCAATAGCTCCAATTGGTATTCGAGG	1020			

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3121 ACCTTTCTTAGCCTTGTCTTGTCCAAATTTGGGCTCATCTAGCTTATCAGCGCCGACTG 3180  
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3121 ACCTTTCTTAGCCTTGTCTTGTCCAAATTTGGGCTCATCTAGCTTATCAGCGCCGACTG 3180

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RESULT 3

LOCUS 125433 6513 bp DNA PAT 03-SEP-1996

DEFINITION Sequence 7 from patent US 5550049.

ACCESSION 125433

NID g1605303

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 6513)

AUTHORS Van Der Ploeg, L.H.T. and Warmke, J.W.

TITLE Process for identifying para cation channel modulators

JOURNAL Patent: US 5550049-A 7 27-AUG-1996;

FEATURES

source Location/Qualifiers

1. .6513

/organism="unknown"

BASE COUNT 1681 a 1548 c 1702 g 1582 t

ORIGIN

Query Match 100.0%; Score 6513; DB 18; Length 6513;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dd	3061	ATGTCTCGTCAATCCCTTCTTCTGGCCACCGTGTCTATCGGCAATCTTGTTGGTACTTA	3120
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QY	3841	AATATCCAGCTGATTGCTGCCCGGATTCGTACTATAGAATAATTCGGATCTTTAGCCGGTG	3900
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4			
RESULT			
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DEFINITION	Drosophila melanogaster para locus, sodium channel alpha subunit		
ACCESSION	M32078 M24285 M32079 M32080		
NID	9403441		
KEYWORDS	alternative splicing; opa repetitive sequence; sodium channel alpha subunit.		
SOURCE	D.melanogaster (strain para-hd2), cDNA to mRNA, clone Z510.3.		
ORGANISM	Drosophila melanogaster		
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 6883)		
AUTHORS	Loughney, K., Kreber, R. and Ganetzky, B.		
TITLE	Molecular analysis of the para locus, a sodium channel gene in Drosophila		
JOURNAL	Cell 58, 1143-1154 (1989)		
MEDLINE	89376565		
REFERENCE	2 (sites)		
AUTHORS	Ramaswami, M. and Tanouye, M.A.		
TITLE	Two sodium channel genes in Drosophila: Implications for channel diversity		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082 (1989)		
MEDLINE	89184571		
REFERENCE	3 (sites)		
AUTHORS	Thackeray, J.R. and Ganetzky, B.		
TITLE	Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms		
JOURNAL	Unpublished (1993)		
COMMENT	Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 86, 1143-1154 (1989)] kindly submitted by B.Ganetzky, 25-APR-1989.		
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CDS

CDS

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Db	375	ATGAAAACGAGAGAGCGTGGAAAGAGAGCCGAGGAGAGTCCCGGATATGGTC	434
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DEFINITION	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds.		
ACCESSION	U38813		
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KEYWORDS	house fly.		
ORGANISM	Musca domestica		
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AUTHORS	Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.		
TITLE	Tight genetic linkage between the kdr insecticide resistance trait and a voltage-sensitive sodium channel gene in the house fly		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)		
MEDLINE	94195766		
AUTHORS	2 (bases 1 to 6318)		
TITLE	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
JOURNAL	Characterization of voltage-sensitive sodium channel gene coding sequences from insecticide-susceptible and knockdown-resistant house fly strains		
MEDLINE	Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)		
REFERENCE	96245434		
AUTHORS	3 (bases 1 to 6318)		
TITLE	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
AUTHORS	4 (bases 1 to 6318)		
TITLE	Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York State Agricultural Experiment Station, Cornell University, Castle Street, Geneva, NY 14456, USA		
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**ORGANISM** *Musca domestica*  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Musca.  
**REFERENCE** 1 (bases 1 to 6899)  
**AUTHORS** Williamson,M.S., Martinez-Torres,D., Hick,C.A. and Devonshire,A.L.  
**TITLE** Identification of mutations in the housefly para-type sodium channel gene associated with knockdown resistance (kdr) to pyrethroid insecticides  
**JOURNAL** Mol. Gen. Genet. 252 (1-2), 51-60 (1996)  
**MEDLINE** 96397509  
**REFERENCE** 2 (bases 1 to 6899)  
**AUTHORS** Williamson,M.S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted, Department of Biological & Ecological Chemistry, Harpenden, Hertfordshire, AL5 2JQ, UK  
**FEATURES** Location/Qualifiers  
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**BASE COUNT** 1965 a 1445 c 1660 g 1929 t  
**ORIGIN**

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QY 2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGGCACAC--CTGTC--TGGA--C-A--CC 2114  
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RESULT 9
LOCUS BGU73583 6096 bp mRNA INV 19-MAR-1997
DEFINITION Blattella germanica para sodium channel mRNA, complete cds.
ACCESSION U73583
NID 91657983
KEYWORDS German cockroach.
SOURCE Blattella germanica
ORGANISM Blattella germanica
Eukaryote; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria;
Blattellidae; Blattellinae; Blattella.
REFERENCE 1 (bases 1 to 6096)
AUTHORS Dong, K.
TITLE A single amino acid change in the para sodium channel protein is
associated with knockdown-resistance (kdr) to pyrethroid
insecticides in German cockroach
JOURNAL Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)
MEDLINE 97218696
REFERENCE 2 (bases 1 to 6096)
AUTHORS Dong, K.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1996) Entomology, Michigan State University, East
Lansing, MI 48824, USA
FEATURES
Location/Qualifiers
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CDS
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BASE COUNT 1615 a 1374 c 1532 g 1575 t

Query Match 29.3%; Score 1910; DB 15; Length 6096;  
Best Local Similarity 71.2%; Pred. No. 0.00e+00;  
Matches 4179; Conservative 0; Mismatches 1579; Indels 115; Gaps 74;  
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[illegible]

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KEYWORDS
SOURCE
ORGANISM
Drosophila virilis
Drosophila virilis
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
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REFERENCE
1 (bases 1 to 2144)
AUTHORS
Thackeray, J.R. and Ganetzky, B.
TITLE
Conserved alternative splicing patterns and splicing signals in the
Drosophila sodium channel gene para
Unpublished (1995)
JOURNAL
2 (bases 1 to 2144)
REFERENCE
Thackeray, J.R. and Ganetzky, B.
AUTHORS
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TITLE
Submitted (04-MAY-1995) Justin R. Thackeray, Biology, Yale
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Note: remainder of annotations omitted.

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Best Local Similarity 90.6%; Pred. No. 0.00e+00;
Matches 1943; Conservative 0; Mismatches 171; Indels 30; Gaps 12;

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Qy 1657 AAGCTACCAAGTTCGTAAGTAGAGCAGCAGATCCTTATCCTTACCTGGTTCCACCGTTTA 1716
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Db      61  ACATACGCAGGGGATCAGTATTCTCAACAAGTACACGATACGTAATGAGCGTGGCCGTT 120
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Note: remainder of annotations omitted.

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Db	181	AACACTTGCATACGCCGATGACTCGAATGCCGTGACGCCAATGTCGAGGAGAAATGGAG	240
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Qy	2977																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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96397510	2 (bases 1 to 5068)	Miyazaki, M., Ohyama, K., Dunlap, D.Y. and Matsumura, F.	
REFERENCE		Direct Submission	
AUTHORS		Submitted (17-SEP-1996)	Environmental Toxicology, University of California at Davis/ITEH, Davis, CA 95616, USA
JOURNAL		Location/Qualifiers	
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		LFQVATFGKWIQIMDAIDSRHLKQPIRENIYKLYFVFIFLPGSFFTLNFIQVI	
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ORIGIN			
Query Match	22.1%	Score 1441; DB 15; Length 5068;	
Best Local Similarity	70.4%	Pred. No. 0.00e+00;	
Matches	3659; Conservative	0; Mismatches 1402; Indels 136; Gaps 81;	
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Db	61	CTAGGAACCTGGCGGCTTCCGAAGCTTCCAGGCTGCTCCGAGCTTTGAAGACTGTCGCT	120
Qy	720	TTAGTAACTAGACGCCCTGCGAAGCTTTAGGCTGCTCGAGCGCTTAAACCGTAGCC	779
Db	121	ATTGTTCCAGTTTGAAGACCATTTGTGGCGCTGTGATTAATCTGTAAGAACCCTGCCG	180
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Db	2362	TTGAACCTCTTCTTGGCCTTGCTGCTCAGCAACTTTGGTTTCACTCCAAATCTGTCAGCCCA 2421
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Db	2422	ACAGCTGACAAATGAACCAACAAGATTGCTGAGGCAATTTGAGGGTTTCTCAGATCTTT 2481
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Qy	3356	AGAGCATGGTGACAAACGAATGGAGCTGGGCCACGACGAGATCCTCGCCAGCCCTCAT 3415
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Qy	3596	TAGAGTTTGTCTTACAGGACGACACACTGCCAGCATTTAACTCATATGCTAGCCATTA 3655
Db	2871	AAACCGTCCATACAGGATGACGCCATAGGGAGTGCAGAGACTATGATGGGAGGA 2930
Qy	3656	GAATCGGCATTCAGGACGAGGCCACAGGGCAGCCGACGACGATGAGGGCGAGGA 3715
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Qy	3716	GAAGCGCAGCCAGCAAGGAGGATTTAGTCTCGACGAGGAACCTGGACGAGGAGGCGA 3775
Db	2991	AGGTGAAGGACCTCTGGAGGAGGACATGGTATTGGATGCAGGCACT - GAGGAGCTCATGA 3049
Qy	3776	ATGCGAGGAGGCGCGCTCGACGGTGTATCATTT - ATTATGACACACGACGAGGATATAC 3834
Db	3050	TGTCAGAAATATCCGCGAGATTGCTCTGATCACTGCTATAGCGCTTCCCTTCCCTTG 3109
Qy	3835	TCGATGAATATCCAGCTGATTGCTGCCCGATTCTGCTACTATAAGAAATTTCCGATCTAG 3894
Db	3110	CTGGAGACGAGACTCTCTTCTTGGCAAGGCTGGGGCAACCTCCGACTGAAACCTTCC 3169
Qy	3895	CGGCTGAGGATGACTCGCGCTTCTGGCAAGGATGGGCAATTTACGACTGAAACACTTTTC 3954
Db	3170	ACTCATTTGAGAACAAATACTTTGAACGGCTGTGATCACCATCATCTCGCTTAGCAGTC 3229
Qy	3955	AATTAATTGAATAATTAATTTGAAACAGCTGTTATCACTATGATTTTATAGTAGCT 4014
Db	3230	TCGCACTGGCCCTTGAGGATGTACATCTGCCTCATCGACCAATTTCTCGAGGACATCTAT 3289
Qy	4015	TAGCTTTGGCATTTAGAAGATGTACATCTGCCCAAAAGACCCATACTCGAGGATATTTAT 4074
Db	3290	ATTACATGGATGATCTTCACTGTCATCTTCAATTTGAGATCTTGATCAAGTGGCTGG 3349
Qy	4075	ACTATATGGACAGAATATTACGGTTATTCTTCTTGGAAATGTTATCACTATGATTTTAT 4134
Db	3350	CCCTTGGTTTCAAAAATAACTTCAAAATGCTTGGTGTGGTGTGGATTTCACTATTCGA 3409
Qy	4135	CGCTCGGCTTCAAAGTGATCTCAACAACGCGTGTGTGGCTCGATTTGCTGATTGTCA 4194
Db	3410	TGGTCTCACATCAFAAACTTCGTAGCAGCCTTGTGGGCGCTTGAGGCAATTCAGCCCTTCA 3466
Qy	4195	TGGTATCGCTTATCAACTTGTGCTTCACTTGTGGAGCTGTGTGATTTCAAGCCCTTCA 4254
Db	3470	AAACTATGAGSACACTCAGGSCCTTAGGCTCTTAGGGCTATGTCTAGAAATCGAGGGA 3529
Qy	4255	AGACTATCGCAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCGTATGCGAGGCA 4314
Db	3530	TGAGGTTGGTGTGAACGCTTTGGTGCAGGCCATCCCCAGTATCTTCTCAATGTGCTCCTCG 3589
Qy	4315	TGAGGTCGTCGTTAATGCGTGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGG 4374
Db	3590	TGTGTCATCTTCTGCTCATCTTTGCCATCATGGGTGCGAGCTGTGTGCTGGGAAAT 3649
Qy	4375	TGTGTCATAATTTTGGCTAATTTTGGCATAATGGGTGTCAGAGCTTTTGTCTGGAAAT 4434
Db	3650	ATCATAAATGTGTGGATTCCAACTCTTACCACCTTTGAGCCACGAATCATCTCTGACAGAA 3709
Qy	4435	ATTTAAGTGGGAGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCA 4494
Db	3710	ATGCTTGCAATTTGTAATAACATACATGAGGAGAACTCGCCAAATGAATTTTGATCATCGTCTG 3769
Qy	4495	ATGCTGTGAGAGGAGAACTTACAGCTGGGTGAATTCAGCAATGAATTTTCGATCATGTAG 4554
Db	3770	GCAAGCTTATCTCTGCTCTTCCAAGTGCCACCTTCAAAGATGGATTCAGATCATGA 3829
Qy	4555	GTACCGCTATCTGTGCTTTTCCAAGTGGCCACTTCAAAGCTGATACAAATCATGA 4614
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Qy	4675	TGTATTTATTTTTCGTATCTTCTCATCATATTTTGGATCCTTTTTCACACTCAATCTGTTC 4734
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Qy	4735	TTGGTGTATTATCATTTAATGAGCAAAAAGAAAGGCAAGGCTGCTGATAGA 4794
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Qy	4795	TGTTCACTGAGAGATCAGAAAAGTACTATAATGCTATGAAGAAATGGGCTCTAAA 4854
Db	4070	AACCGTTAAAAGCCATCCCGAGGCAAGTGGAGACCGGAGCCACTTGTGTTGAAATCT 4129
Qy	4855	AACCATTAAGGCCATTCCAAGACCAAGTGGCGACCAAGCAATAGTCTTTCAAATAG 4914
Db	4130	GCACAGACAAGAAATTTGACATGATCATGTTGTTCAATTTGGCTTTTAACTGTTTAAACA 4189
Qy	4915	TAAACGATAAGAAATTCGATATAATCATTTATTTTCAATTTGGTCTGAACATGTTTCAACA 4974
Db	4190	TGACTCTGATCTCATCAACAGTCAAGACAGTTTCAGGACGCTTCTTGATTTACTTGAACA 4249
Qy	4975	TGACCTCGATCGTTACGATGGTGGACACGATGAACGCGCTCTAGACTATCTCATG 5034
Db	4250	TGATCTTCATCTCATCTTCCAGTCTCGAGTCTGATGAAGATATTCGCCCTCAGATACC 4309
Qy	5035	CGATATTCGTAGTTTATTTTTCAGTTCCGAATGTCTATTAATAATATTCGTTTACGATATC 5094
Db	4310	ACTACTTCAAGAAACCATGGACCTCTTTGATTTTCGTAGTTGTCTATCTATATTGG 4369
Qy	5095	ACTATTTTATTGAGCCATGGAAATTTATTTGATGTAGTTAGTTGTCATTTTATCCATCTTAG 5154



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Qy 3441 CAACCTGGAGGTGGCCATCGGGGATCGGATGGAATTCAGTACACGGCGACATGAAGAAC 3500
Db 841 AACAGCCCAAGAAATCAAAATCTTAAATAACAACACGATGATTTGGAAACTCAATAAAC 900
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Qy 3561 CACCAAGACATAGACTGGACACGAGCTAAACCATAGAGTTTGTCCATACAGGACGAC 3620
Db 961 GACACTGCCAGCATTAATCTCATATGG 986
Qy 3621 GACACTGCCAGCATTAATCTCATATGG 3646

RESULT 13
LOCUS 083874 986 bp mRNA INV 07-APR-1998
DEFINITION Haematobia irritans para-like sodium channel (HF-para-like) mRNA,
alternatively spliced, partial cds.
ACCESSION U83874
NID 92231550
KEYWORDS horn fly.
SOURCE Haematobia irritans
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Haematobia.
REFERENCE 1 (bases 1 to 986)
AUTHORS Guerrero.F.D., Jamroz.R.C., Kammlah.D. and Kunz.S.E.
TITLE pyrethroid-resistant horn flies, Haematobia irritans:
Toxicological and molecular characterization of
pyrethroid-resistant horn flies, Haematobia irritans:
identification of kdr and super-kdr point mutations
Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
JOURNAL 98105586
MEDLINE 2 (bases 1 to 986)
REFERENCE Guerrero.F.D., Jamroz.R.C. and Kunz.S.E.
AUTHORS Direct Submission
TITLE Submitted (06-JAN-1997) USDA-ARS, Knippling-Bushland Livestock
JOURNAL Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
TX 78028, USA
FEATURES
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ORIGIN

Query Match 10.7%; Score 694; DB 15; Length 986;
Best Local Similarity 85.2%; Pred. No. 0.00e+00;
Matches 840; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Qy 2661 GAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCGTATTGGAAGTGGGACTC 2720
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Db 61 GAAGGTGTCAGGGGCTTCCGCTGTTAAGAGTTTTCGTTTTCGTTGCTTCAAAATTG 120
Qy 2721 GAGGGTGCCAGGGGCTGTGTCGGTATTGCGTTCCTTCGATGTCGGTGTATTCAAACTG 2780
Db 121 GCAAAATCTTGGCCACACCTGAACTTACTTCAATTTAGGGCCGCGACAAATGGGTGCA 180
Qy 2781 GCCAAGTCTTGGCCACACACTTAAATTTACTTCAATTTAGGGACGACCACTGGCGCT 2840
Db 181 TTGGGTAAATCTAACATTTGTACTTTGCAATTAATCATCTTTCATCTTTGCGGTATGGGAATG 240
Qy 2841 TTGGGTAAATCTGACATTTGTACTTTGCAATTAATCATCTTTCATCTTTGCGGTATGGGAATG 2900
Db 241 CAACCTTTTCGGAAGAACTATATTGATCACAGGACAAATTCAAAGATCATGAATTAATCT 300
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Qy 2961 CGTGGAACTTTCACGACTTTATGACAGCTTCATGATCGTTCGCGGTGCTCTGCGGA 3020
Db 361 GAATGATTAATCCATGTCGAGTGCATGATGTGGGCGATGTCCTCTGTATACCAATTC 420
Qy 3021 GAATGATCGAGTCCATGTCGAGTGCATGATGTGGGCGATGTCCTCTGTATACCAATTC 3080
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Qy 3081 TTCTTGGCCACCGCTTTCATCGCAATCTGTGGTACTTTTAAACCTTTTCTTACTGCTT 3140
Db 481 TTCTCCTCAATTTTCGTTTCACTAGTTTATCAGCACCGACTGCGGACAAATGATACCAATAA 540
Qy 3141 TTCTCCTCAATTTTGGCTCATCTAGCTTATCAGCGCGACTGCGGATACGATACGATTA 3200
Db 541 ATACGAGAGCCCTTCAATCGTATTTCTCTTTAAGAACTGGGTGAAACGTAATATTGCC 600
Qy 3201 ATACGCGAGCCCTTCAATCGAATTTGGCCGATTTAAAGTTTGGGTAAAGCGTAATATTGCT 3260
Db 601 GATTGTTTAAAGTTAATAGCTAATTAATGACAAATCAAAATAGTGACCAACCATCAGGT 660
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Db 661 GAGAGGATCAACGAGATCAGTTGGATTGGAGCGAAGAACATGCGGATTAATGAATGGAG 720
Qy 3321 GAGAGGATCAACGAGATCAGTTGGATTGGAGCGAAGAACATGCGGATTAATGAATGGAG 3380
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Qy 3381 CTGGGCCACGACGAGATCTCTCGCCGACGGCTCATCAAGAAGGGGATCAAGGAGCAGACG 3440
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Qy 3441 CAACCTGGAGTGGCCATTTGGCGGATGGGATGGAATTCACGATCACCGGACATGAAGAAC 3500
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Db 961 GACACTGCCAGCATTAATCTCATATGG 986
Qy 3621 GACACTGCCAGCATTAATCTCATATGG 3646

RESULT 14
LOCUS DMU26715 1840 bp DNA INV 30-APR-1996
DEFINITION Drosophila melanogaster sodium channel protein (para) gene,
optional segments f and h, partial cds.
ACCESSION U26715
NID g1110473
KEYWORDS fruit fly.
SOURCE
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ORGANISM Drosophila melanogaster  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1840)  
AUTHORS Thackeray, J.R. and Ganetzky, B.  
TITLE Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms  
J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)

JOURNAL MEDLINE 94238327  
REFERENCE 2 (bases 1 to 1840)  
AUTHORS Thackeray, J.R. and Ganetzky, B.  
TITLE Conserved alternative splicing patterns and splicing signals in the Drosophila sodium channel gene para  
Genetics 141 (1), 203-214 (1995)

JOURNAL MEDLINE 96042905  
REFERENCE 3 (bases 1 to 1840)  
AUTHORS Thackeray, J.R. and Ganetzky, B.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA

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BASE COUNT 673 a 374 c 305 g 488 t

Query Match 7.4%; Score 485; DB 15; Length 1840;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1311 TCGACCATTCGAAGCAGCAGACCAAGGGCAGCGCCGAGACGATGGAGCGCAGAGGAA 1370  
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Db 1371 CGCGCAGCCAGCAGGAGGATTTAGTCTCGACGAGAACTGGACGAGGAGCGGAATG 1430  
Qy 3719 CGCGCAGCCAGCAGGAGGATTTAGTCTCGACGAGAACTGGACGAGGAGCGGAATG 3778

Db 1431 CGAGGAGGCGCGCTCGACGTGATATCATATTCATGTCACACACGAGGATATACTCGA 1490  
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Db 1491 TGAATATCCAGCTGATGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGG 1550  
Qy 3839 TGAATATCCAGCTGATGCTGCCCGGATTCGTACTATAAGAAATTTCCGATCTTAGCCGG 3898

Db 1551 TGACGATGACTCCCGCTTCTGCGAAGGATGGGCAATTTACGACTGAAACTTTTCAATT 1610  
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Db 1611 AATTGAAAATAAATATTTTGAACACAGCTGTATCACTATGATTTTAAATGAGTAGCTTAGC 1670  
Qy 3959 AATTGAAAATAAATATTTTGAACACAGCTGTATCACTATGATTTTAAATGAGTAGCTTAGC 4018

Db 1671 TTTGG 1675  
Qy 4019 TTTGG 4023

RESULT 15  
LOCUS U83871 947 bp mRNA INV 07-APR-1998  
DEFINITION Haematobia irritans para-like sodium channel (HF-para) mRNA, alternatively spliced, partial cds.  
ACCESSION U83871  
NID 92231544  
KEYWORDS horn fly.  
SOURCE Haematobia irritans  
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia.  
REFERENCE 1 (bases 1 to 947)  
AUTHORS Guerrero, F.D., Jamroz, R.C., Kammlah, D. and Kunz, S.E.  
TITLE Toxicological and molecular characterization of pyrethroid-resistant horn flies, Haematobia irritans: identification of kdr and super-kdr point mutations  
Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)  
JOURNAL MEDLINE 98105586  
REFERENCE 2 (bases 1 to 947)  
AUTHORS Guerrero, F.D., Jamroz, R.C. and Kunz, S.E.  
TITLE Direct Submission  
JOURNAL Submitted (06-JAN-1997) USDA-ARS, Knippling-Bushland Livestock Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville, TX 78026, USA

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BASE COUNT 273 a 181 c 207 g 286 t

ORIGIN

Query Match 6.9%; Score 448; DB 15; Length 947;  
Best Local Similarity 84.0%; Pred. No. 0.00e+00;  
Matches 553; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Db 1 GAGGCGTGAATATTTTCGATTTCAATATCGTTGCGCTTGTCTTCTTACTGGAATGGGCGTG 60  
Qy 2661 GAGGCGTGAATATTTTCGATTTCAATATCGTTGCGCTTGTCTTCTTACTGGAATGGGCGTG 2720

Db 61 GAAGGCTCCAGGCGTGTCCGTGTTAAGAAGTTTCGTTTGTCTTCTGTTATTCAAATG 120  
Qy 2721 GAAGGCTCCAGGCGTGTCCGTGTTAAGAAGTTTCGTTTGTCTTCTGTTATTCAAATG 2780



